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Matches 1788; Conservation 0.000-001; Indexes 0; Gaps 0;

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[illegible]









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 Magnoliophyta; eudicotyledons; Rosales; Brassicaceae;  
 Arabidopsis.  
 REFERENCE 1 (bases 1 to 108056)  
 AUTHORS Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brannon, R.C.,  
 Mason, T.M., Kerlavage, A.R., Adams, M.P., Somerville, C.R. and  
 Venter, J.C. thaliana 'TAMU' BAC 'T29E15' genomic sequence near  
 marker 'C1C06C07'  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 108056)  
 AUTHORS Rounsley, S.D. and Lin, X.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JUN-1998) The Institute for Genome Research, 9712  
 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org  
 On Sep 16, 1998 this sequence version replaced g13601085.  
 COMMENT \*\*\* WARNING: Phase 2 High Throughput Genome Sequence \*\*\*  
 \*\*\* This sequence is unfinished. It consists of 1 contigs for  
 which the order is known. The lengths of the gaps have been  
 \* estimated by the submitter but are not known exactly. When  
 \* sequencing is complete, the sequence data presented in this  
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 ACCESSION T22011  
 NID g1602365  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 85)  
 AUTHORS Keene, J.D., Levine, T. and Gao, F.  
 TITLE Methods and compositions useful in the regeneration, binding and  
 expression of ribonucleic acids involved in cell growth, neoplasia  
 and immunoregulation  
 JOURNAL Patent: US 5525495-A 97 11-JUN-1996;  
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 KEYWORDS HTG.  
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 Eudicotyledons; Rosales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (sites)  
 AUTHORS Nakamura, Y.  
 TITLE Structural Analysis of Arabidopsis thaliana Chromosome 5. IV  
 JOURNAL Unpublished (1998)  
 REFERENCE 2 (bases 1 to 80376)  
 AUTHORS Nakamura, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-JAN-1998) The Plant TMBI/GenBank databases,  
 Yashuhiro Nakamura, Fudan University Institute Laboratory of  
 Gene Structure 2, 1027, Yanchi, Kuzhuo, China 202, Japan  
 (E-mail: ynakamura@fudan.ac.cn, Tel: 81-438-52-3935,  
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ACCESSION  Y13098
KEYWORDS   32230822
SOURCE     Dictyostelium discoideum.
ORGANISM   Dictyostelium discoideum.
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            1 (bases 1 to 1100)
            Williams, J.G.
            Direct Submission
            Submitted (09-MAY-1997)  J.G. Williams, MBL Laboratory for Molecular
            Biology and Dept of Biochem, MBL, P.O. Box 9, Woods Hole, MA 01984
            2 (bases 1 to 1100)
            Robinson, V. and Williams, J.G.
            A marker of terminal stalk cell terminal differentiation in
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            Unpublished
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DEFINITION A.thaliana mRNA for peroxidase, prxr10.
ACCESSION  X98322
KEYWORDS   a1402899
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            1 (bases 1 to 1289)
            Capellin, N., Tognelli, M., Flach, J., and Le, S., French Institute for
            and Simon, P.
            Flaven cDNA clones from Arabidopsis thaliana encoding
            isoperoxidases (Accession Nos. X98318, X98319, X98320, X98321, X98322 and X98423)
            Plant Physiol 112, 446-448 (1996)
JOURNAL

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ردیف	نام و نام خانوادگی	تاریخ تولد	تاریخ فوت	محل تولد	محل دفن	توضیحات
۱	محمد علی...	۱۳۰۲/۰۵/۰۵	۱۳۸۵/۰۳/۱۵	تهران	تهران	
۲	علیرضا...	۱۳۰۳/۰۶/۱۰	۱۳۸۶/۰۴/۲۰	تهران	تهران	
۳	فریدون...	۱۳۰۴/۰۷/۲۰	۱۳۸۷/۰۵/۱۰	تهران	تهران	
۴	مهدی...	۱۳۰۵/۰۸/۰۵	۱۳۸۸/۰۶/۲۵	تهران	تهران	
۵	سید علی...	۱۳۰۶/۰۹/۱۵	۱۳۸۹/۰۷/۱۵	تهران	تهران	
۶	محمدرضا...	۱۳۰۷/۱۰/۲۵	۱۳۹۰/۰۸/۲۰	تهران	تهران	
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Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5





\_\_\_\_\_

100

































SOURCE Human.  
 ORGANISM Homo sapiens.  
 EUROPEAN STR. Haploids, embryonic, Metazoa, Chordata.  
 Vertebrata, Euteleostei, Pilichthys, Catfish, Homio.  
 REFERENCE 1 (Bases 1 to 496)  
 AUTHORS Berry, P. J., Stevens, J. Z., Walter, N. A. R., Wilcox, A. S., Putnam, T. H.,  
 Hopp, J. A., & Walter, J. C. 1995. P. J. Stevens, M. E. and J. A. Z. M.  
 TITLE Gene-based sequence-tagged sites (STSs) as the basis for a human  
 gene map.  
 JOURNAL Nature Genet. 10, 415-423 (1995)  
 MEDLINE 95430922  
 COMMENT  
 CONTACT: Sikela TM  
 Department of Pharmacology  
 University of Colorado Health Sciences Center  
 BOX 350671, Denver, CO 80262-0671, Tel: 303-755-7022  
 FAX: 303-755-7027  
 Email: nikola@hsc.uchsc.edu  
 Seq primer: 21M13 Universal  
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 \*\*\*\*\*  
 WSEARCHING v.2.0 - n.d. database search, using Smith-Waterman algorithm  
 Run on: Tue Jan 19 11:54:33 1999, 950.352 Million cell updates/sec  
 Tabular output not generated.  
 Title: >US-08-955-841-1  
 Description: (1-1789) from US08955841.seq  
 Percent Score: 1789 1 CAAATGATATCTTCTGATGAT  
 N.W. Sequence: CTTAAGTAGAGCTGATGGA  
 Comp: ..AAAAAAGAAAAAAGAAAAA 1789  
 ..TTTTTTTTTTTTTTTTTT  
 Scoring table: TABLE (metric  
 Gap 60  
 Nmatch: STD: Dbase 0: Query 0  
 Searched: 18642 seqs, 1864249 bases x 2  
 Post-processing: Minimum Match 0%  
 Listing first 45 summaries  
 Database: n-database32  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
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 \*\*\*\*\*  
 WSEARCHING v.2.0 - n.d. database search, using Smith-Waterman algorithm  
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14 25 1.4 495 38 V03892  
 15 25 1.4 615 38 V02881  
 16 25 1.4 882 35 T72173  
 17 25 1.4 940 13 Q85268  
 18 25 1.4 1590 3 C15023  
 19 25 1.4 1703 39 V04774  
 20 25 1.4 1872 15 Q90617  
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 22 25 1.4 1872 40 V15216  
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 34 25 1.4 2330 43 V15704  
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 38 25 1.4 2734 5 Q39221  
 39 25 1.4 2781 4 Q25712  
 40 25 1.4 2781 2 Q13239  
 41 25 1.4 3192 1 Q06055  
 42 25 1.4 3521 7 Q41230  
 43 25 1.4 3521 7 Q41236  
 44 25 1.4 3785 35 T79275  
 45 25 1.4 3956 35 T79274

## ALIGNMENTS

RESULT 1  
 ID T1716 standard: cDNA: 1786 BP.  
 AC T1716;  
 DI 29-SEP-1997 (first entry)  
 DE Human integrin-linked kinase (ILK) cDNA.  
 KW Integrin-linked kinase; ILK; serine/threonine kinase; cell growth;  
 KW cell adhesion; cell migration; cell invasion; inhibitor;  
 KW gene therapy; diagnosis; cancer; leukaemia; tumour; inflammation;  
 KW arthritis; osteoporosis; cardiovascular disease; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 Key 157..1512  
 cds  
 FT polyA\_signal 1749..1754  
 FT /\*tag= a  
 FT /\*tag= b  
 FT W09723625-A1.  
 PD 03-JUL-1997.  
 PE 19-NOV-1996; CA0760.  
 PR 21-DEC-1995; US-009074.  
 PA (DEDH/) DEDHAR S.  
 FA (HANN/) HANNIGAN G.  
 PI Dedhar S, Hannigan G;  
 PF WP: 97-351062/12  
 PP P-PSDB: W18211.  
 DR New isolated integrin-linked serine/threonine kinase, cloned  
 E1 develop products to modulate cell growth, adhesion, migration and  
 E2 invasion, e.g., for treating cancer or inflammation  
 E3 Claim 3; Fig. 1a, 6pp; English.  
 E4 cDNA clone Plac5 (T1716) codes for a serine/threonine kinase  
 E5 (Wisc1) which is an integrin-linked kinase, designated ILK,  
 E6 that can be used to modulate cell growth, adhesion, migration and  
 E7 invasion. It was isolated from a human placental cDNA library  
 E8 using a partial cDNA, B17-9, that had been obtd. in a two-hybrid  
 E9 screen using a bait plasmid expressing the integrin beta-1 subunit  
 E10 cytoplasmic domain. The ILK chromosomal locus has been mapped to  
 E11 11p15, a region implicated in a subset of breast carcinomas,  
 E12 inherited cardiac arrhythmia and long QT syndrome. ILK nucleic





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12 FEB-1996 (first entry)
DE Zeamatin synergistic antifungal protein coding sequence.
KW Zeamatin; synergistic antifungal protein; fungicide; pesticide;
OS transgenic plant; disease-resistance; SS.
FH Key Location/Qualifiers
FT misc_feature 19..21
FT /**tag= a
FT /note= "star" code for Zeamatin coding sequence"
FT /**tag= b
FT /note= "first codon of mature Zeamatin protein"
PI W09527791-A1.
PI 13-JUN-1995.
PI 04 JAN-1995; U00432.
PI 10-JAN-1994; US-178708.
PI (CIBA) CIBA GEIGY AG.
PI (UYKE-) UNIV RFS CORP.
PI Lane BE, Potter SL, Roberts WK, Solitrennikoff GP.
PI P-PSDB, 875930.
PI DNA encoding Synergistic Anti-Fungal Protein - obtained from coho.
PI sorghum and oat, used in synergistic compsns. against fungi and
PI yeasts, e.g. Neurospora and Candida.
PI Claim 5; Page 47-48; 58pp, English.
CC Zeamatin cDNA may be obtained using standard DNA techniques, and may
CC be expressed under the control of the constitutive 35S promoter; it
CC transgenic plants - plants expressing high Zeamatin levels have
CC enhanced resistance to plant pathogens. Zeamatin, and other
CC synergistic antifungal proteins (SAFPs), synergize with fungicide
CC antibiotics such as nikkomycin. Alone, they display fungicidal
CC activity against fungi including Neurospora and Trichoderma. Yeasts
CC e.g. Candida and plant pathogenic fungi, including Phytophthora,
CC Clactomium and Fusarium.
CC N.B. On decoding this cDNA sequence, the complete Zeamatin protein
CC sequence given in SEQ ID NO.4 is not obtained.
SQ Sequence 894 bp. 267 G; 277 C; 144 T;
Query Match 1.5%; Score 26; 1H 16; Length 84;
Best Local Similarity 100.0%; Pred. No. 7,000-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 864 attatgaaataaaataaaataaa 894
|||||
OY 1762 ATTATGAAAAAATAAAATAAA 1767
RESULT 7
ID T08171 standard: cDNA: 1408 bp.
AC T08171;
DE 23-MAY-1996 (first entry)
DE Full length coconut LPAAT clone 94104.
KW Lysophosphatidic acid acyl transferase; coconut; medullosa plant; LPAAT
KW 1-acyl glycerol-3-phosphate acyltransferase; aryl-esterase; LPAAT
OS Fungi; biotechnology; modification; triacylglyceride; acyl transferase; SS.
AS Cocos nucifera.
FH Key Location/Qualifiers
FT cds 259..1182
FT /**tag= a
FT /product= coconut LPAAT
PI W09527791-A1.
PI 19-OCT-1995.
PI 31-MAR-1995; U03997.
PI 06-APR-1994; US-224625.
PI 21-APR-1994; US-231196.
PI 06-JUN-1994; US-254404.
PI 21-OCT-1994; US-327451.
PI (CALJ) CALGENE INC.
PI Davies HW, Hawkins D, Lassner M, Nourse J.
PI WPI: 95-366394/47.
PI P-PSDB; R87723.
PI Plant lysophosphatidic acid acyl transferase - used to manufacture
PI fatty acid compsns. from biosynthesized LPAAT.

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12 FEB-1996 (first entry)
DE Zeamatin synergistic antifungal protein coding sequence.
KW Zeamatin; synergistic antifungal protein; fungicide; pesticide;
OS transgenic plant; disease-resistance; SS.
FH Key Location/Qualifiers
FT misc_feature 19..21
FT /**tag= a
FT /note= "star" code for Zeamatin coding sequence"
FT /**tag= b
FT /note= "first codon of mature Zeamatin protein"
PI W09527791-A1.
PI 13-JUN-1995.
PI 04 JAN-1995; U00432.
PI 10-JAN-1994; US-178708.
PI (CIBA) CIBA GEIGY AG.
PI (UYKE-) UNIV RFS CORP.
PI Lane BE, Potter SL, Roberts WK, Solitrennikoff GP.
PI P-PSDB, 875930.
PI DNA encoding Synergistic Anti-Fungal Protein - obtained from coho.
PI sorghum and oat, used in synergistic compsns. against fungi and
PI yeasts, e.g. Neurospora and Candida.
PI Claim 5; Page 47-48; 58pp, English.
CC Zeamatin cDNA may be obtained using standard DNA techniques, and may
CC be expressed under the control of the constitutive 35S promoter; it
CC transgenic plants - plants expressing high Zeamatin levels have
CC enhanced resistance to plant pathogens. Zeamatin, and other
CC synergistic antifungal proteins (SAFPs), synergize with fungicide
CC antibiotics such as nikkomycin. Alone, they display fungicidal
CC activity against fungi including Neurospora and Trichoderma. Yeasts
CC e.g. Candida and plant pathogenic fungi, including Phytophthora,
CC Clactomium and Fusarium.
CC N.B. On decoding this cDNA sequence, the complete Zeamatin protein
CC sequence given in SEQ ID NO.4 is not obtained.
SQ Sequence 894 bp. 267 G; 277 C; 144 T;
Query Match 1.5%; Score 26; 1H 16; Length 84;
Best Local Similarity 100.0%; Pred. No. 7,000-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 864 attatgaaataaaataaaataaa 894
|||||
OY 1762 ATTATGAAAAAATAAAATAAA 1767
RESULT 7
ID T08171 standard: cDNA: 1408 bp.
AC T08171;
DE 23-MAY-1996 (first entry)
DE Full length coconut LPAAT clone 94104.
KW Lysophosphatidic acid acyl transferase; coconut; medullosa plant; LPAAT
KW 1-acyl glycerol-3-phosphate acyltransferase; aryl-esterase; LPAAT
OS Fungi; biotechnology; modification; triacylglyceride; acyl transferase; SS.
AS Cocos nucifera.
FH Key Location/Qualifiers
FT cds 259..1182
FT /**tag= a
FT /product= coconut LPAAT
PI W09527791-A1.
PI 19-OCT-1995.
PI 31-MAR-1995; U03997.
PI 06-APR-1994; US-224625.
PI 21-APR-1994; US-231196.
PI 06-JUN-1994; US-254404.
PI 21-OCT-1994; US-327451.
PI (CALJ) CALGENE INC.
PI Davies HW, Hawkins D, Lassner M, Nourse J.
PI WPI: 95-366394/47.
PI P-PSDB; R87723.
PI Plant lysophosphatidic acid acyl transferase - used to manufacture
PI fatty acid compsns. from biosynthesized LPAAT.

```

Example 2: Fig 13: 127bp; English.  
 Gene: 1564bata0312.001 and transposon (LPAT, 89718-03) cloned  
 11 Tricyclitol 3-phosphate acyltransferase (AG3PAT) from coconut or  
 12 membranes have the characteristics of being free from cytoplasmic  
 13 proteins of the plant. They possess 131 activity, towards an acyl-CoA  
 14 donor substrate and contain the peptide sequences 88701-17. The peptide  
 15 sequences were used to design oligonucleotide primers and probes for  
 16 isolation of AG3PAT clones from coconut and meadowfoam cDNA libraries.  
 17 The nucleic acids can be used to isolate other AG3PAT gene which encode  
 18 protein with biotechnological applications such as modification of plant  
 19 triacylglyceride compounds.  
 20 The nucleotide sequence of the full length coconut LPAT clone COLP4,  
 21 the sequence encodes a protein of 308 amino acid with a calculated mol.  
 22 wt. of 31.8 kD that is consistent with the observed mass of 27-29 kD by  
 23 SDS-PAGE). The protein has a calculated pI of 9.79. The gene was  
 24 isolated from a coconut endosperm cDNA library using probes derived from  
 25 amino acid sequencing of the protein such as 108157-8 or using PCR  
 26 amplified fragment of the gene such as fragments 18161-8  
 27 Sequence 1408 BP: 377 A: 212 C: 221 G: 401 T:  
 28  
 Query Match: 1.53, Score 26, DB 17, Length 1409,  
 Best Local Similarity 96.38, Pred. No. 7,00e-05,  
 Mismatches 20, Conservative 0, Mismatches 1, Indels 0, Gaps 0.  
 29 1521 tatgataaataaataaataaataaataa 1347  
 30 1 1111111111111111111111111111  
 31 1763 TATGATAAATAAATAAATAAATAAATAA 1789  
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drug targeting: ss.  
 Homo sapiens.  
 Location/Qualifiers  
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 /product= human alpha IFN  
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 226..234  
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 WC0105632-A.  
 12-MAY-1991.  
 19-OCT-1990: F00758.  
 20-OCT-1989: FP-013770  
 (CNPS ) CNPS CENT NAT PECH SCI.  
 Mogensen KE, Use G, Luttalla G, Gresser I:  
 WFE 91:148740/20.  
 P-PSDB; R11958.  
 New human alpha-interferon receptor protein - useful for testing  
 PI Interferon agonists and in treatment or diagnosis  
 PS Disclosure; fig 4; 30pp; French.  
 CC This sequence encodes a recombinant human alpha interferon (IFN)  
 CC receptor protein useful for the testing of IFN agonists and for  
 CC treatment and diagnosis of viral diseases and tumours. Antibodies  
 CC raised against this protein can be used for blocking the receptor  
 CC when required, e.g. where overexpression of alpha IFN is harmful.  
 CC The Abs are also useful for e.g. drug targeting. Variants of the  
 CC protein, having residue 164 (Thr) replaced by Ala and an Asp in-  
 CC serted between residues 472 and 490, are also useful.

















[illegible]



[illegible]

```

11 4255702 (first entry)
12 Sequence of Drosophila heat shock factor (HSF) cDNA.
13 Bsp. shock factor; stress condition; assay; ss.
14 Drosophila.
15 Key: 100% Ids/Qualifiers
16 225..235
17 /*ad a
18 2723..2728
19 /*ad b
20 2723..2728
21 /*ad b
22 Wt: 617 A.
23 225..235
24 225..235
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99 225..235
100 225..235

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PT in living systems.
PS Dislosure: Fig 2; 68pp; English.
CC The sequence encodes Drosophila heat shock factor protein and was
CC obtained by screening a Drosophila genomic library with oligo-
CC nucleotide probes (Q13237, Q13238) based on the HSF amino acid
CC sequence. The HSF sequence can be used to identify the HSF genes in
CC other organisms and also for the detection of stress or a diseased
CC state in living systems. The gene can be used to increase
CC expression of other gene prods. by cotransfecting the HSF gene
CC together with other genes linked to heat shock elements. It can be
CC linked to a tissue-general or tissue-specific promoter and
CC introduced into transgenic mice as a tool for eliciting increased
CC or chronic stress response conditions as a model for how tissues
CC respond to chronic stress conditions such as those caused by viral
CC infection, chemical or mechanical stress. See also Q1240 and
CC Q13241.
SQ Sequence 2781 BP; 831 A; 631 C; 690 G; 629 T;

Query Match 1.4%; Score 25; DB 1; Length 2781;
Best Local Similarity 100.0%; Pred. No. 3.50e-04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0

LE 2754 atgaaataaaataaaataaaataaaataaa 2778
|||||
QY 1765 ATGAAAAAATAAAATAAAATAAAATAAA 1789

RESULT 41
ID G05055 standard; DNA; 3192 BP.
AC G05055;
DI 24-JAN-1991 (first entry)
DE 5'-sequence of yeast plasmid pVK11.
KE Beta-galactosidase; lacA; pVK11; ds.
OS Saccharomyces cerevisiae.
FH Key
FT cds
FT Location/Qualifiers
FT 11..3028
FT /*tag= a
FT W09010703-A.
FT 20-SEP-1990.
PF 13-MAR-1990; G00373.
PR 13-MAR-1990; GR-005674.
PA (UNLO ) IMPERIAL COLLEGE SC.
PI Hartley BS, Ramakrishnan S, Kumar V;
DR WPI: 90-305026/40.
DR P-PSDB: R07114.
PT DNA construct contg. beta-galactosidase gene and yeast promoter
PT and transformed yeast cells able to ferment lactose in whey
PS Dislosure: Fig 2; 35pp; English.
CC Claimed sequence includes a Beta-galactosidase lacA gene from
CC Aspergillus niger and the Acl1 yeast promoter in plasmid vector
CC pVK11. The plasmid is used to transform a yeast expression system to
CC produce BG extracellularly or into the periplasmic space, useful in
CC fermenting lactose to produce EtOH.
SQ Sequence 3192 BP; 773 A; 874 C; 786 G; 759 T;

Query Match 1.4%; Score 25; DB 1; Length 3192;
Best Local Similarity 100.0%; Pred. No. 3.50e-04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 3151 atgaaataaaataaaataaaataaaataaa 3175
|||||
QY 1765 ATGAAAAAATAAAATAAAATAAAATAAA 1789

RESULT 42
ID Q41230 standard; DNA; 3521 BP.
AC Q41230;
DI 02-SEP-1993 (first entry)
DE Gene encoding major surface gp of rat P. carinii.
KE Major surface glycoprotein; gp116; rat; Pneumocystis carinii.
KW vaccine; HIV; human immunodeficiency virus; diagnostic; gp; ss.
OS Rat Pneumocystis carinii.
FH Key
FT Location/Qualifiers

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\*\*\*\*\*

WATERMAN

(TW)

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MPsearch\_n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Thu Jan 14 23:13:22 1999; MasPar time 2892.42 Seconds  
1363.044 Million cell updates/sec  
Tabular output not generated

Title: SUS-08-955-641-1  
Description: (1-1789) from US08955841.seq  
Perfect Score: 1789  
N.A. Sequence: 1 GAATTCATCTGCGACTGCT  
Comp: CTTAAGTAGACAGCTGACGA

Scoring table: TABLE Default  
Gap 5

Nmatch STD : Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb155

1:em\_ba 2:em\_fun 3:em\_htg 4:em\_hum1 5:em\_hum2 6:em\_in  
7:em\_m 8:em\_or 9:em\_ov 10:em\_pat 11:em\_ph 12:em\_pl  
13:em\_ro 14:em\_v1  
Database: genbank107  
15:ab\_ba1 16:ab\_ba2 17:ab\_ba3 18:ab\_ba4 19:ab\_ba5 20:ab\_ba6  
21:ab\_ba7 22:ab\_ba8 23:ab\_ba9 24:ab\_ba10 25:ab\_ba11  
26:ab\_ba12 27:ab\_ba13 28:ab\_ba14 29:ab\_ba15 30:ab\_ba16 31:ab\_ba17  
32:ab\_ba18 33:ab\_ba19

Statistics: Mean 11.810 Variance 8.232 scale 1.435

Pred. No is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1787	99.9	1789	26	H5U40282 Homo sapiens integrin-	0.00e+00
2	1336	74.7	1750	28	MMU94479 Mus musculus integrin	0.00e+00
3	129	11.1	232	30	human STS A002040, seq	9.79e-93
4	177	9.9	2605	26	Human TATA-binding pro	7.76e-93
5	72	4.0	7218	21	Sequence 14 from patent	1.34e-30
6	46	2.6	7218	21	Sequence 14 from patent	1.86e-07
7	33	2.2	74371	25	Homo sapiens chromosome	3.25e-04
8	39	2.2	74371	25	Homo sapiens chromosome	3.25e-04
9	35	2.0	3531	25	Human SH3 domain-conta	1.88e-02
10	35	2.0	3558	25	Human protein kinase	1.88e-02
11	35	2.0	216021	26	HUAC004787 Homo sapiens	1.88e-02
12	34	1.9	404	23	Sequence 21 from patent	5.03e-02
13	34	1.9	800	23	Nicotiana tabacum b1p3	5.03e-02

14	1451	26	AF013988	Homo sapiens serine pr	5.03e-02
15	2873	27	AF048986	Homo sapiens Mts homo	5.02e-02
16	19	5909	18	MEMA2C4A A.suum alpha-2 (iv) co	5.02e-02
17	34	8145	28	MMANK1AA Mus musculus Ank-1 mPNA	5.03e-02
18	32	85	21	Sequence 97 from patent	3.47e-01
19	32	215	21	Sequence 97 from patent	3.47e-01
20	33	565	21	QUA encoding envelope	1.33e-01
21	32	1161	18	Bactrocera papayae str	3.47e-01
22	32	3520	28	MMANK1AC Mus musculus Ank-1 mPNA	3.47e-01
23	32	6192	25	MMANK1AC Mus musculus Ank-1 mPNA	3.47e-01
24	32	6238	28	Human erythroid ankyrin	3.47e-01
25	32	7252	25	Mouse red cell ankyrin	3.47e-01
26	32	238500	17	Human mRNA for ankyrin	3.47e-01
27	31	215	21	Human DNA sequence	3.47e-01
28	31	551	18	Sequence 97 from patent	9.91e-01
29	30	486	30	Strongyloides stercora	9.91e-01
30	30	979	20	Epilp735 Human chromos	2.26e-00
31	31	1139	18	CGATA-3 Chickens, liv	2.26e-00
32	30	1162	18	Bactrocera quadriseos	8.91e-01
33	30	1162	18	Bactrocera papayae str	2.26e-00
34	30	1162	18	Bactrocera carambolae	2.26e-00
35	30	1296	18	Acanthokara kaptensis	2.26e-00
36	30	1493	23	Chit44-endochitinase	9.91e-01
37	30	1667	26	Human clone 2385 mPNA	2.26e-00
38	30	1755	23	Arabiopsis thaliana	2.26e-00
39	30	3298	19	Cryptotagus punctatus	2.26e-00
40	30	3713	28	MMALPA Mus musculus alpha-actin	2.26e-00
41	30	7251	18	Plasmodium falciparum	2.26e-00
42	30	76848	17	Plasmodium falciparum	2.26e-00
43	30	104810	26	Human PAC clone 1714	2.26e-00
44	31	125295	27	Homo sapiens chromosom	9.91e-01
45	31	216021	26	HUAC004787 Homo sapiens	8.91e-01
46	31	224645	17	AC004153 *** SEQUENCING IN PROG	8.91e-01

ALIGNMENTS

1	HSU40282	1789 bp	mPNA	PPI	21-MAY-1998
LOCUS	Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.				
DEFINITION	U40282				
ACCESSION	93150001				
NID	human.				
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Ekaryotae, mitochondrial eukaryotes, Metazoa, Chordata:				
REFERENCE	1 (bases 1 to 1789)				
ATTNOPS	Radeva, G., Filmus, J., Bell, J. C. and Dedhar, S.				
TITLE	Regulation of cell adhesion and anchorage-dependent growth by a new				
JOURNAL	beta 1-integrin-linked protein kinase				
MEDLINE	Nature 379 (6560), 91-96 (1996)				
REFERENCE	2 (bases 1 to 1789)				
AUTHORS	Dedhar, S. and Hannigan, G. E				
TITLE	Direct Submission				
JOURNAL	Submitted (07-NOV-1995) Shoukat Dedhar, Cancer Biology Research,				
REFERENCE	Sunnybrook Health Science Centre and University of Toronto, 3075				
AUTHORS	Bayview Avenue, North York, Ont. M4N 3M5, Canada				
TITLE	3 (bases 1 to 1789)				
JOURNAL	Dedhar, S. and Hannigan, G. E.				
REFERENCE	Submitted (21-MAY-1998) Shoukat Dedhar, Cancer Biology Research,				
AUTHORS	Sunnybrook Health Science Centre and University of Toronto, 3075				
TITLE	Bayview Avenue, North York, Ont. M4N 3M5, Canada				
JOURNAL	Sequence update by submitter				
REFERENCE	07 May 20, 1998 This sequence version replaced 9315004173.				
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AUTHORS	/chromosome="11"				
TITLE	/map="11p15"				

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/ly:lv:st:fn:fv:ds:qv:af:ka:ld:ma:rg:ma:fl:ht:le:pl:pr:hl:ns:rv:ml:de:mt:ar											
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Qy	121	TCGCCAATCCAGGGAGTCTGGGCGCGGAC	GGTGTGATGGAGACATTTTCACTCAGTGC	180							
Dk	181	CGGAGGAGGACGACGTCGCGGTCGCTGT	GGCTGGACGAGGAGGACGACCTCAAC	240							
Qy	181	CGGAGGAGGACGACGTCGCGGTCGCTGT	GGCTGGACGAGGAGGACGACCTCAAC	240							
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Dk	481	TTTGGGGCCACATCAAGTGGGAGGACCT	GGTGGCAATGGGGCCCTTCTCAGCATC	540							
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Qy	541	TGTAACAGTATGGAGAGATGCTGTGGACA	AGCCAAAGCCACCCCTCGAGAGGCTTCT	600							
Dk	601	CGACAGGAGGACATCAAGATGGGAGGAC	ATCTCAACCGTATTCATACAGGACATTC	660							
Qy	601	CGACAGGAGGACATCAAGATGGGAGGAC	ATCTCAACCGTATTCATACAGGACATTC	660							
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Qy	661	TGGAAGGAGGACATCAAGATGGGAGGAC	ATCTCAACCGTATTCATACAGGACATTC	720							

[illegible]



CP 497 TGAATCTGGGCCCCAA 487

REFERENCE: 2 (Pages 1 to 43/1)  
AUTHORS: Picke, D.O.

CP 497 TGAATCTGGGCCCCAA 487

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TITLE      Large Scale Sequence Analysis and Annotation with the Sequence
REFERENCE  Comparison Analysis (SCAN) System
JOURNAL    3 (bases 1 to 74371)
AUTHORS    Kimmerly,W., Bondar,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Davis,C.A., Kadner,K., Miguel,T., Pflueck,S., Pollard,M.,
            Rojkeski,H., Subramanian,S. and Martin,C.H.
TITLE      Direct Submission
JOURNAL    Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome
            Institute, Lawrence Berkeley National Laboratory, MS 74-157,
            Berkeley, CA 94720, U.S.A.
COMMENT    Sequence submitted by:
            DOE Joint Genome Institute.
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                        /note="100% identity EST v084a10.x1"
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Note: remainder of annotations omitted.

Query Match 2.28; Score 39, DB 26; Length 74371;  
Best Local Similarity 11.88; Pred. No. 3,25e-04;  
Matches 26; Conservative 106; Mismatches 87; Indels 1; Gaps 1;

Db 15923 STKSCMSRSPKSPGYPYKYPKPCAMMTCKSSKWCWSYRMRMKYSCSYCYCSSG 15982  
QY 870 GIGHCGGCTCAGGATTTTCGGATCAATGTCCTCCAGTCTAGTCCCTGCCA 929

Db 15983 KKYWCRCSMYTYCYKYSKYKYSMSYCTCTSGWRWMMKSGRSMYASRSGSCSCSMCM 16042  
QY 930 GTCTCCACCTGCTCCTCCTACTCTCATCACACACTGATGCCGCTATGATCCCTCA 989

Db 16043 MCRCSCMSKMMWMTTITTKTRTWTTTWKRWKAGASASRGSKRCMSYKSKSTCKMK-M 16101  
QY 990 CAATGTACTACATGAGGCCACCAATTTCGTGGACCAAGCCAGCGCTGGAAGTTGC 1049

Db 16102 TCYGMYSWCSYKMYKSYRCCGCGCYSSSYCKSCCWMMSMR 16141  
QY 1050 ITTGGACATGCAAGGAGGCAAGGCTTCTCTACACACACTA 1089

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RESULT 8
LOCUS AC005369 74371 bp DNA PRI 01-AUG-1998
DEFINITION Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
sequence.
ACCESSION AC005369
NID 93367505
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 74371)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,

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```

Kadner,K., Miguel,T., Miller,C., Pittluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
Sequencing of human chromosome 5
Unpublished
REFERENCE 2 (bases 1 to 74371)
AUTHORS Ricker,D.O.
TITLE Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 74371)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Davis,C.A., Kadner,K., Miguel,T., Pittluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
DIRECT SUBMISSION
TITLE Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
COMMENT Sequence submitted by:
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[illegible]

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complete cds.
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NID g454027
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SOURCE
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 3531)
GALLOK A., Mark, M.R., Scadden, D.T., Wang, Z., Gu, Q. and
Godowski, P.J.
IDENTIFICATION AND CHARACTERIZATION OF SPPK, A NOVEL SRC-HOMOLOGY 3
DOMAIN-CONTAINING PROLINE-RICH KINASE WITH SERINE/THREONINE KINASE
ACTIVITY.
J. Biol. Chem. 269, 15092-15100 (1994)
94253068
MEDLINE 2 (bases 1 to 3531)
AUTHORS Godowski, P.J.
DIRECT SUBMISSION
TITLE Submitted (15-MAR-1994) Paul J. Godowski, Genentech, Inc., 460
Point San Bruno Blvd., South San Francisco, CA 94080, USA
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AVQIARGMYLHCEALVPIHFDLKNLILQPTESDDMEHKTLTITDGLAREWHK
ITOMSAAGTYANMAPEVIKASTFSKGSQWFGVLLMELLITGEVYRGIDCLAVAYG
AVNKLITPISCTPEPAQLMADCAQDPHRRPOFASITLOQLEAEQVLUREMPDPS
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EVEREELTILIOQVPEPHKVEELTRKPKSLRPAQGGEPISMLDEKHPITVQASP
GLDPRNRNVEVGGSGSTPPFRFAIQLEPAEQGQAWGRTSPPLDESSNGEPACQAW
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577, 756
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793, 1659
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Best local Similarity -83.0%; Pred. No. 1.88e-02;
Matches 44; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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[illegible]

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BASE COUNT      287 a   131 c   199 g   183 t
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Best Local Similarity 94.7%; Pred. No. 5.03e-02;
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 755 TCAGATGAAGTTTACATGAAAAAAGAAAAAAGAAAAA 796
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1748 TCACATAAAGTTTATGAAAAAAGAAAAAAGAAAAA 1789

RESULT 14
LOCUS AF013988 1451 bp mRNA PRI 12-AUG-1997
DEFINITION Homo sapiens serine protease mRNA, complete cds
ACCESSION AF013988
NID g2318114
KEYWORDS
SOURCE human.
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Homi-
nidae; Homo.
REFERENCE 1 (bases 1 to 1451)
AUTHORS Little, S.P., Johnson, E.M., Dixon, E.P., Norris, F., Buckley, W.,
Becker, G., Johnson, M., Dobbins, J.R., Wyrick, T., Miller, J.R.,
Mackellar, W., Hepburn, D., Corvalan, J., McClure, D., Liu, X.,
Stephenson, D., and Clemens, J.
Zyme cDNA isolated from AD brain tissue
J Biol Chem (1997); In press
REFERENCE 2 (bases 1 to 1451)
AUTHORS Little, S.P., Johnson, E.M. and Norris, F.
Direct Submission
Submitted (15-JUL-1997) CNS Division, Eli Lilly and Company, Lilly
Corporate Center, Indianapolis, IN 45285, USA
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PTHUGELSPLEVTQFFLPNLMWAM; HPIIHKINPLIKEMKLSHKVSEWQ
VLYKTVSALGPLCA; PSLP; SI; LFFIAQEI; SLLHIA; SLKGVVDFEGLAENK
FTVLPNIDPEIDEKPPPLGSPFLTEVAKPFIENIDSPSCSVIYIPLIGLISIP
RLPSMVEASDFEINGLDMFLSEELKHPSPAPIKELDALGLHCE; IPIQETLLMYQL
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ELCARTFVNSTECGGDKPVVITGNSSGKSIYKQVGLIFMALVGSFVPAEEAE
IGAVDAIFTRHSCSISIGLSIFMDLNLQVAKVNNATAUSLVLDIFGKGINVDG
LALLAAVLEHMLAPGTPCHIEVATNPLSVLQIIPQGLPVYLTMETEGNGLVF
FYV; EGVAVASHASHIAAAGLLEKLVAPGVSEVLLIPSGVETPVRKLI; LPPN; MEN
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BASE COUNT      675 a   774 c   753 g   671 t
ORIGIN
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Best Local Similarity 94.7%; Pred. No. 5.03e-02;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2835 AATAAGTTTATTGAGAAAAAAGAAAAAAGAAAAA 2872
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Qy 1752 AATAAGTTTATTGAGAAAAAAGAAAAAAGAAAAA 1789

Search completed: Fri Jan 15 00:02:01 1999
Job time : 2919 secs.

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WILEY

(TM)

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Distribution rights by Oxford Molecular Ltd

MPSrch\_nnn n a - n a database search, using Smith-Waterman algorithm  
Pss On: Fri Jan 15 09:47:22 1999; MasPar time 243.09 Seconds  
Tabular output not generated. 830.444 Million cell updates/sec

Title: >US-08-955-841-1  
Description: (1-1789) from US08955841.seq  
Perfect Score: 1789  
N A Sequence: 1 GAATTCATCTGCGACTGCT  
Comp: CIIAAGTAGACATGACGA

Scoring table: TABLE default  
Gap 5

Nmatch STD: Dbase 0; Query 0

Searched: 128442 seqs, 58026449 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39 40:part40

Statistics: Mean 9.634; Variance 6.948; scale 1.386

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1768	98.8	1786	32	Human integrin-linked	0.00e+00
2	47	2.6	204	1	Base substituted Eco	5.09e-10
3	45	2.5	91	9	Oligonucleotide probe	4.81e-09
4	40	2.2	21	9	Oligonucleotide probe	1.18e-06
5	39	2.2	204	1	Base substituted Eco	3.49e-06
6	38	2.1	114	12	Generic DNA sequence	1.02e-05
7	36	2.0	114	12	Generic DNA sequence	8.51e-05
8	35	2.0	114	12	Generic DNA sequence	2.43e-04
9	34	1.9	114	12	Generic DNA sequence	6.85e-04
10	34	1.9	114	12	Generic DNA sequence	6.85e-04
11	34	1.9	114	12	Generic DNA sequence	6.85e-04
12	34	1.9	114	12	Generic DNA sequence	6.85e-04
13	34	1.9	404	8	PKC gene LpK4 partia	6.85e-04

14	34	1.9	404	16	T03098	Protein tyrosine-kinase	5.85e-04
15	32	1.8	85	23	T39470	Growth regulatory pro	5.29e-02
16	33	1.8	114	12	Q70472	Generic DNA sequence	1.91e-03
17	33	1.8	114	12	Q70472	Generic DNA sequence	1.91e-03
18	33	1.8	114	12	Q70472	Generic DNA sequence	5.29e-03
19	33	1.8	114	12	Q70472	Generic DNA sequence	5.29e-03
20	33	1.8	114	12	Q70472	Generic DNA sequence	5.29e-03
21	31	1.7	114	12	Q70456	Generic DNA sequence	1.45e-02
22	31	1.7	114	12	Q70456	Generic DNA sequence	1.45e-02
23	31	1.7	114	12	Q70471	Generic DNA sequence	1.45e-02
24	31	1.7	114	12	Q70470	Generic DNA sequence	1.45e-02
25	31	1.7	178	32	T76405	Human endothelin-1 an	1.45e-02
26	30	1.7	178	32	T76405	Human endothelin-1 an	3.91e-02
27	30	1.7	654	29	T47675	Human G protein gamma	3.91e-02
28	30	1.7	766	37	N40132	Sequence of Prepropr	3.91e-02
29	30	1.7	1755	37	T31321	Arabidopsis thaliana	3.91e-02
30	30	1.7	2589	30	T61590	Human c-IAP1	3.91e-02
31	29	1.6	565	6	Q35072	HCV envelope region p	1.04e-01
32	29	1.6	1229	15	Q85932	CDNA encoding Lol pV	1.04e-01
33	29	1.6	1239	6	Q38329	Sequence of ryc grass	1.04e-01
34	29	1.6	1239	1	N01576	Sequence of alpha 1B	1.04e-01
35	29	1.6	1239	3	Q33000	Sequence encoding ryc	1.04e-01
36	29	1.6	1239	7	Q43439	Lol pI CDNA clone 1B	1.04e-01
37	29	1.6	1376	10	Q56747	Ryegrass Lol pV aller	1.04e-01
38	29	1.6	1562	7	Q42769	Ligand-induced gene	1.04e-01
39	29	1.6	1836	33	T84277	Mouse Flt4 receptor t	1.04e-01
40	28	1.6	1873	5	Q38736	Mouse osteogenic pro	2.74e-01
41	29	1.6	2211	2	Q22190	Human sperm-specific	1.04e-01
42	29	1.6	2400	31	T49364	Nicotiana plumbaginif	1.04e-01
43	29	1.6	2784	2	Q11701	Human alpha-interfero	1.04e-01
44	29	1.6	4673	4	Q37189	P. Yoelii SSP2 antiag	1.04e-01
45	29	1.6	6877	10	Q53548	Cinnamyl alcohol dehy	1.04e-01

## ALIGNMENTS

RESULT 1  
ID T71716 standard; CDNA; 1786 BP.  
AC T71716.  
DE 29-SEP-1997 (first entry)  
KW Human integrin-linked kinase (ILK) CDNA.  
KW Integrin-linked kinase; ILK; serine/threonine kinase; cell growth;  
KW cell adhesion; cell migration; cell invasion; inhibitor;  
KW gene therapy; diagnosis; cancer; leukemia; tumor; inflammation;  
KW arthritis; osteoporosis; cardiovascular disease; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT cds 157..1512  
FT poly\_a\_signal 1749 1754  
FT /\*tag= a  
FT /\*tag= b  
FN WO9723625-A1.  
PD 03-JUL-1997.  
PF 19-NOV-1996; CA0760.  
PP 21-DEC-1995; US-009074  
PA (DEH/) DEHAP S.  
PA (HANN/) HANNIGAN G.  
PI Dedhar S., Hannigan G.  
DR WPI: 97-351062/32.  
DR P-PSDB: W18211.  
DE New isolated integrin-linked serine/threonine kinase - used to  
DE develop products to modulate cell growth, adhesion, migration and  
DE invasion e.g. for treating cancer or inflammation  
PS Claim 3; Fig 1a; 6pp; English.  
CC CDNA clone Plac5 (T71716) codes for a serine/threonine kinase  
CC (W18211) which is an integrin-linked kinase, designated ILK,  
CC that can be used to modulate cell growth, adhesion, migration and  
CC invasion. It was isolated from a human placental cDNA library  
CC using a partial CDNA, BIT-9, that had been obtd in a two-hybrid  
CC screen using a bait plasmid expressing the integrin beta-1 subunit  
CC cytoplasmic domain. The ILK chromosomal locus has been mapped to  
CC 11p15, a region implicated in a subset of breast carcinomas,  
CC inherited cardiac arrhythmia and long QT syndrome ILK nuclei

acids (including antisense) can be used in gene therapy to inhibit  
 tk expression for the treatment of e.g. cancer, leukemia, solid  
 tumor, chronic inflammatory disease, arthritis, osteoporosis and  
 cardiovascular disease, and can also be used as diagnostics to  
 screen biopsy samples.

Sequence 1786 BP: 443 A: 487 C: 479 G: 377 T:

Quality Match 98.8%: Score 1768; DB 32; Length 1786;

Best Local Similarity 40.8%: Pred No. 6 matches;

Matches 1786; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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 1 GAATTCATTATGAGATGCTATCAGGGAGGTTCGGGGAAAGATCCTGAGCGGAGGT 60  
 61 ccgagagataaagctgaggttcatcctcctcctggatcactccacagctcctcagct 120  
 61 CCGAGAGATAAAGCTGAGGTTTCACTCCTCCTCGGATCACTCCACAGCTCCTCAGCT 120  
 121 tcccccaatccagggagctcggcccgaggagctgctgctatgagacattttcactcagtc 180  
 121 TCCCCCAATCCAGGGAGCTCGGCCGAGGAGCTGCTGCTATGAGACATTTTCACTCAGTC 180  
 181 cggag 240  
 181 CGGAG 240  
 241 cag 300  
 241 CAG 300  
 361 gtgatttaatttgaatcagtcgggggggagagagagagagagagagagagagagagag 360  
 361 GTGATTTAATTTGAATCAGTCGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 421 tacaaag 420  
 421 TACAAAG 420  
 481 ttttgag 540  
 481 TTTTGAG 540  
 601 cag 660  
 601 CAG 660  
 721 gacttcacacagcttaactcctgacacagagagagagagagagagagagagagagag 780  
 721 GACTTCACACAGCTTAACCTCCTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 841 aag 900  
 841 AAG 900  
 961 ataaag 1020  
 961 ATAAAG 1020

401 AATGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 460  
 461 acacacag 1020  
 1021 gacacacag 1080  
 1081 gacacacag 1140  
 1141 gacacacag 1200  
 1201 gacacacag 1260  
 1261 gacacacag 1320  
 1321 gacacacag 1380  
 1381 gacacacag 1440  
 1441 gacacacag 1500  
 1501 gacacacag 1560  
 1561 gacacacag 1620  
 1621 gacacacag 1680  
 1681 gacacacag 1740  
 1741 gacacacag 1800  
 1801 gacacacag 1860  
 1861 gacacacag 1920  
 1921 gacacacag 1980  
 1981 gacacacag 2040  
 2041 gacacacag 2100  
 2101 gacacacag 2160  
 2161 gacacacag 2220  
 2221 gacacacag 2280  
 2281 gacacacag 2340  
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 2521 gacacacag 2580  
 2581 gacacacag 2640  
 2641 gacacacag 2700  
 2701 gacacacag 2760  
 2761 gacacacag 2820  
 2821 gacacacag 2880  
 2881 gacacacag 2940  
 2941 gacacacag 3000

RESULT 2

ID N81164 standard; DNA; 204 BP.

AC N81164;

DT 08-Nov-1990 (first entry)

EF Base substituted F coli beta-galactosidase alpha-fragment.

KW E.coli beta galactosidase alpha-fragment, base substitutions: ss.

OS Escherichia coli.

PH Key Location/Qualifiers

FT misc\_feature 19 69

FT /\*tag= a

FT /\*tag= b

FT primer\_bind 187..204

FT primer\_bind 187..204

FT primer\_bind 187..204

PN EP-285123-A.



ID	Q51746 standard; cDNA, 91 BP.
AC	Q51746;
DT	31-MAY-1994 (first entry)
DE	Oligonucleotide probe MK14-A
DE	Oligonucleotide, DNA probe, mycobacteria, disease diagnosis;
KW	ss.
OS	Synthetic.
PN	EP-571911-A.
PD	01-DEC-1993.
PF	24-MAY-1993; 108325.
PP	26-MAY-1992; UA-889651.
PP	(BECT ) BECTON DICKINSON CO.
PI	Shank LD, Spears PA;
PI	WPT: 93-378044/8
PT	New oligo:nucleotide probes specific for Mycobacteria : used for
PT	detection and amplification of Mycobacteria nucleic acid in
PT	samples
PS	Claim 3; Page 14; 23pp; English.
PS	Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC	(Q51745) it hybridized to all spp. of mycobacteria tested, but
CC	cross reacted to a few non-mycobacterial spp. The probe may
CC	be useful as an initial screen for mycobacterial infection
CC	See also Q51735-45 and Q51747-59.
CC	Sequence 91 BP: 5 A: 17 C: 15 G: 4 T:
SQ	

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Query Match      2.2%, Score 40, DP 2, Length 21;
Best Local Similarity 8%; Prd No. 1 198-06;
Matches          3; Conservative 43; Mismatches 5; Indels 0; Gaps 0;

Db       7 ggcggssvhsyyvvshhhshhythrvhvsvvvvhbvbbbhbyygv    59
|||
CP       1400 GTTCGATGCAAGTGAAGAAGTTTCTAATCATTAACTTAATCAATCCCA   34
```

```

RESULT      5
ID      N81164 standard: DNA; 204 BP.
AC      N81164:
DE      08-NOV-1990 (first entry)
DT      Base substituted E.coli beta-galactosidase alpha-fragment.
DT      E.coli beta galactosidase alpha-fragment; base substitutions: S.
KW      Escherichia coli.
OS      Escherichia coli.
Key      Location/Qualifiers
FT      misc_feature      19..69
FT      CDS
FT      CDS
FT      primer_bind      /*tag= a
FT      primer_bind      /*function=multiple cloning site
FT      primer_bind      187..204
FT      primer_bind      /*tag= b
FT      EP-285123-A.
PN      05-MAY-1988.
PD      30-MAR-1988; 105163.
PD      03-APR-1987; US-034819.
PA      (SUSO) SUOMEN SOKERI OY.
PI      Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen I;
PI      WPI: 88-279927/40.

```

PT Introducing random point mutations into nucleic acids -  
PT by prep of single stranded template, annealing a primer, elongation,  
PT misincorporation, completion of molecules and screening.  
PS Disclosure: p: English.  
CC Random point mutations were introduced into the alpha fragment of  
CC E.coli beta-galactosidase. The wild type sequence was obtained as a  
CC single stranded template and an oligonucleotide was hybridised to  
CC it to generate a popn of DNA molecules which terminate at all  
CC possible nucleotide positions within a specified region. The  
CC variable 3' ends generated in this way are used as primers for  
CC reverse transcriptase. Nucleotides are misincorporated by the  
CC transcriptase and the molecules are completed to forms that can be  
CC amplified and then expressed in a suitable host-vector system.  
CC The sequence covers all 176 diff base substitutions, most of which  
CC occurred singularly in any given mutant.  
CC See also P80575.

Query Match: 3.28; Score 39; DB 1; Length 204;

[illegible]





KW paraneoplastic sensory neuropathy; oncoprotein; lymphokine; rat  
KW RNA recognition motif; RRM; Drosophila; cellular growth; localiza-  
KW instability, translatability, neurons, autoantigenic protein, FE, F











Query Match 99.18; Score 99.18; P-Val 1.00e-148;  
Best Local Similarity 99.18; Pred. No. 0.00e+00;



[illegible]











Tel: (301) 496-1550  
 Email: Robert\_Strausberg@nih.gov  
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Stratagene, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 cDNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/btrp/image/image.html](http://www.bio.lnl.gov/btrp/image/image.html)

Insert Length: 1458 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 315.

## FEATURES

Location/Qualifiers  
 1..491  
 /organism="Homo sapiens"  
 /note="Organ: Kidney; Vector: Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Pooled kidney tumors. 5' adaptor sequence: 5' GAATCGGCACGAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' Average insert size: 1.0 kb."  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1574295"  
 /clone\_lib="NCI-CGAP\_Kid6"  
 /sex="mixed"  
 /tissue\_type="kidney tumor"  
 /lab\_host="SOLR (kanamycin resistant)"  
 111 a 130 c 134 g 116 t

BASE COUNT  
 ORIGIN

Query Match 23.5%; Score 420; DB 15; Length 491;  
 Best Local Similarity 95.5%; Pred. No. 0.00e+00;  
 Matches 472; Conservative 0; Mismatches 16; Indels 6; Gaps 5;

Db 1 GCGGGGGTATCCCTCCCATGTTGTAGACACCATGTGGCAAGTGACAAAGCTCTGAGC 60  
 Cp 1745 GGTGGGGTATCCCTCCCATGTTGTAGACACCATGTGGCAAGTGACAAAGCTCTGAGC 1686

Db 61 GCGGGGGTATCCCTCCCATGTTGTAGACACCATGTGGCAAGTGACAAAGCTCTGAGC 120  
 Cp 1685 GGTGGGGTATCCCTCCCATGTTGTAGACACCATGTGGCAAGTGACAAAGCTCTGAGC 1629

Db 121 GAATTCATGACTGAGCGGGGAGCAACACAGAGGCTCTGCTTTGGGAGGTGCA 180  
 Cp 1628 GTAGTACCATGACTGAGCGGGGAGCAACACAGAGGCTCTGCTTTGGGAGGTGCA 1569

Db 181 TTGCGCCCAACCATGTCCTCCGACACCTCTGGAGTTAGGCAAGGACCTTCCAGTCTACTTG 240  
 Cp 1558 TTGCGCCCAACCATGTCCTCCGACACCTCTGGAGTTAGGCAAGGACCTTCCAGTCTACTTG 1509

Db 241 TCTGTATCTTCTCAGGATAGGCAATCATGTCAAATTTGGTGGCTTTGCAGGGTCT 300  
 Cp 1508 TCTGTATCTTCTCAGGATAGGCAATCATGTCAAATTTGGTGGCTTTGCAGGGTCT 1449

Db 301 TCATTCATGAGATCTTCATGAGCTTACACATGAGGGGAAATACCTGCTGGATGTA 360  
 Cp 1448 TCATTCATGAGATCTTCATGAGCTTACACATGAGGGGAAATACCTGCTGGATGTA 1389

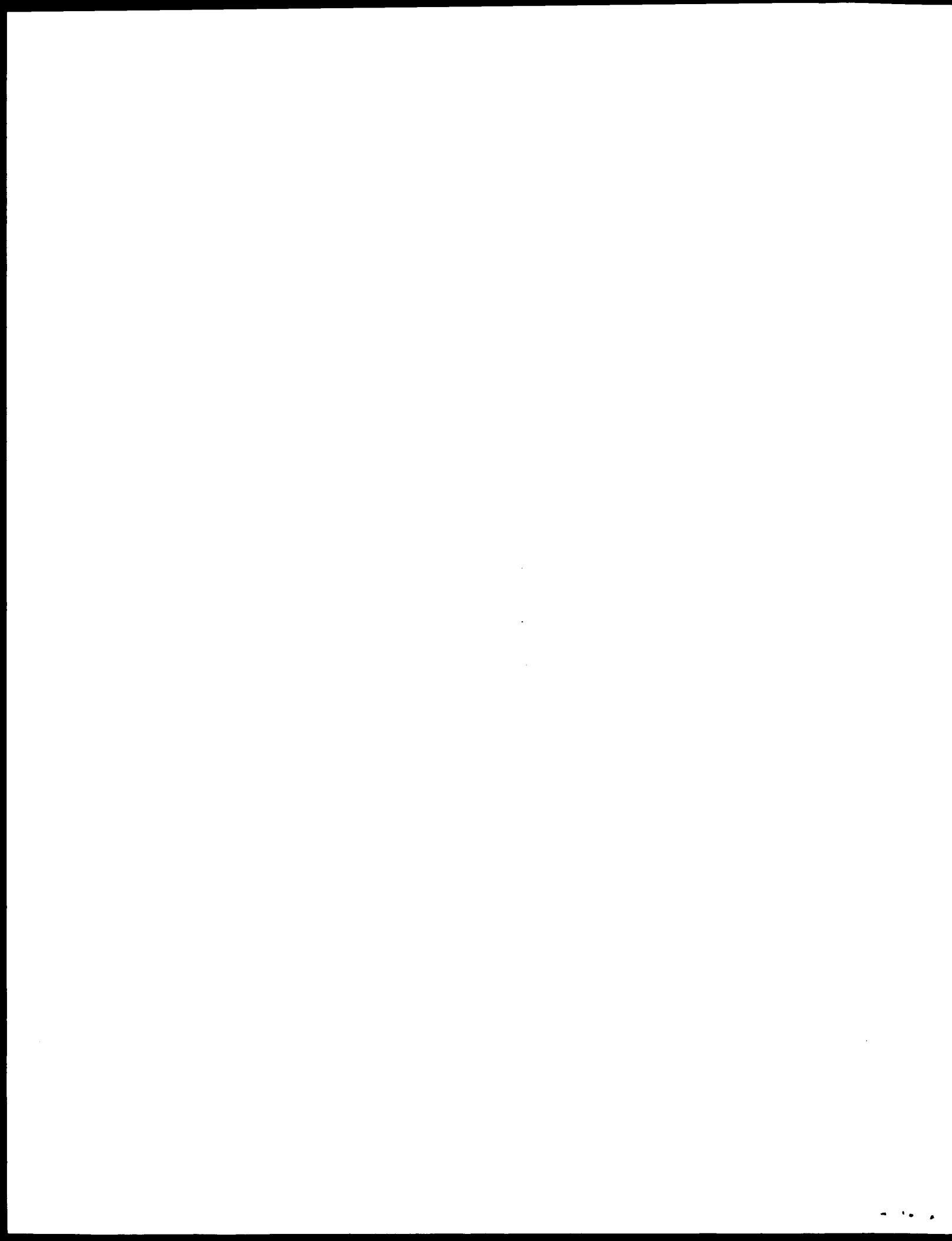
Db 361 GCGGACTTAC--CAATGCGACCTTCATTCCTCAATTCCTATTTGGAGAGGTGCAAAAG 417  
 Cp 1388 GCGGAAAGGCTTTCATTCCTCAATTCCTCAATTCCTATTTGGAGAGGTGCAAAAG 1329

Db 418 GGTACTCCCTGTGTCCACGATATCCAGAGGACCTGCAAACTCCACATGCTGCTGAG 477  
 Cp 1328 GGTACTCCCTGTGTCCACGATATCCAGAGGACCTGCAAACTCCACATGCTGCTGAG 1269

Db 478 GGTCTGTTGTGTC 491  
 Cp 1268 GGTCTGTTGTGTC 1255

Search completed: Fri Jan 15 09:47:00 1999

Job time : 2678 secs.











DB R10932: R24466  
 PT Receptor-like tyrosine kinase reactive with monoclonal antibody  
 PT L11A4 - is Eph-A2-like kinase, useful for phosphorylating  
 PT proteins in modulating pre-B, B and T cell function, in cancer  
 PT therapy etc  
 PS Claim 6: Fig 1: 589p: English.  
 CC This sequence is identical to human EphA2-like kinase (HEK) is  
 CC expressed in both pre-B cells and T cell lines and in a number of  
 CC tumors of human origin. Q1 lymphoid tumors IK63, Ila-1 and IM.  
 CC and the epithelial tumor Hela. This receptor-type tyrosine kinase  
 CC (EphA2) is a member of the protein-tyrosine kinase family. The  
 CC production and/or function of pre-B, B and T cells. The IK and its  
 CC analogues have activity in transducing signals or in stimulating  
 CC cellular responses such as growth and/or differentiation.  
 CC Sequence 983 AA:  
 S0  
 Query Match 9.58; Score 321; DB 6; Length 983;  
 Best Local Similarity 27.84; Pred. No. 5.07e-18; Indels 17; Gaps 16;  
 Matches 57; Conservative 60; Mismatches 92;  
 DB 260 valtllksgytkkprkfbcasimgzfdhpnir-icgvwtkskp-mminteymngs 706  
 QY 217 IYVVKVKESTKSTKSTKSTKSTKSTKSTKSTKSTKSTKSTKSTKSTKSTKSTK 276  
 DB 707 iustirkuadgltvkgmgtlrlglsykykysdmsrwhrdlaaralllnstgkpr 762  
 QY 277 LYNVLH-ESLNEVLE-AYVFALEMAWMAFLHLEFLPRHNLNRSVWIDETAPI 335  
 DB 763 sdlsrsvleupduyrtkygkplwtscslarfkfcsasdvsgyglvkwmsy 821  
 QY 336 smlavkifqcfcmvafanvafec-vfwdtn-pp--sa-dmshfavlwlvi-r 388  
 DB 822 gllpkmqgdlv-akrldgplrkfssfnalglglwkwkdnrrpvcogivslrk 880  
 QY 389 EYFPADLSNMECHVALEGLRTFTFQISPHVCKIMKCNMDEPAKPKKDMIVPILEK 448  
 DB 881 I 881  
 QY 449 M 449  
 RESULT 8  
 ID R14275 standard; Protein: 516 AA.  
 AC R14275.  
 DI 09-JAN-1992 (first entry)  
 DE Sequence encoded by human OT18 clone pHEP1-B  
 DB Homo sapiens.  
 PS Homo sapiens.  
 PS 58760035 A.  
 PD 10-SEP-1991.  
 PE 09-AUG-1990: 560035.  
 PR 09-AUG-1990: 75-840015.  
 PA (USSH ) NAT INST OF HEALTH.  
 PI Miki T, Aaronson SA, Fleming I;  
 DR WPI 91-010283/12.  
 DR N-PSDB: Q14048.  
 PT New genetic cloning vectors - which provide efficient, automatic  
 PT directional cloning of cDNA 3' ends of a eukaryotic mRNA.  
 PS Disclosure: Fig 9: 108pp: English.  
 CC The sequence was deduced from a clone isolated from a cDNA library  
 CC prepared in a new cloning vector (lambda phage). The library was  
 CC prepared from RNA extracted from a secondary transformant of a  
 CC thymoma-induced tumour, OT18. The N-terminal portion of the  
 CC protein contains an unknown sequence but the C-terminus appears to  
 CC be closely related to human B-raf product.  
 CC See also R14280.  
 CC Sequence 516 AA:  
 S0  
 Query Match 9.4%; Score 318; DB 3; Length 516;  
 Best Local Similarity 28.2%; Pred. No. 5.07e-18;  
 Matches 72; Conservative 72; Mismatches 91; Indels 20; Gaps 16;  
 DB 219 gtvkakwhg-dvavkmlnvctppqqlqaknevgvirknrlmlng-y-stk-pg 274  
 QY 296 GELNKGWQGDIVVKVVKVPEWSTFKSFENECPKLRFSHNVLFVIGACUSTFIR 324  
 DB 275 laivtqwcgsslyhhilietkfi--chaklkldfdringmdyhrkafkrlr 324  
 QY 295 FLIIHWPYSLYNLHE-GINFWVDS-AYVFALEMAWMAFLHLEFLPRHNLNRS 324  
 DB 331 niflbedtkvkgdglatvksrwsghqeqsluslhwdevarvdkakpysf 324  
 QY 324 SWIIEEDTARIS---MADVNFSEU-C-I-GKMAFA-NVAFALAEFLHLEFLPRHNLNRS 324

DB 275 laivtqwcgsslyhhilietkfi--chaklkldfdringmdyhrkafkrlr 324  
 QY 296 GELNKGWQGDIVVKVVKVPEWSTFKSFENECPKLRFSHNVLFVIGACUSTFIR 324  
 DB 275 laivtqwcgsslyhhilietkfi--chaklkldfdringmdyhrkafkrlr 324  
 QY 295 FLIIHWPYSLYNLHE-GINFWVDS-AYVFALEMAWMAFLHLEFLPRHNLNRS 324  
 DB 331 niflbedtkvkgdglatvksrwsghqeqsluslhwdevarvdkakpysf 324  
 QY 324 SWIIEEDTARIS---MADVNFSEU-C-I-GKMAFA-NVAFALAEFLHLEFLPRHNLNRS 324  
 DB 451 rderplfpqilasie 465  
 QY 433 PAKRPFDMIVPILE 447  
 RESULT 9  
 ID R10932 standard; Protein: 516 AA.  
 AC P10932;  
 DI 09-MAY-1991 (first entry)  
 DE T18 oncogene prod.  
 KW B-raf; OT18; tumour; hepatoma.  
 OS Mus musculus.  
 FH Key Location/Qualifiers  
 FT protein 1..188  
 FT /label= unknown sequence  
 FT 189..516  
 FT /label= B-raf-related gene prod.  
 PT WO9102077-A.  
 PD 21-FEB-1991.  
 PE 30-JUL-1990: 504239.  
 PR 28-JUL-1989; US-386053.  
 PA (USDC ) US SEC OF COMMERCE.  
 PI Miki T, Aaronson SA, Fleming I;  
 DR WPI 91-073549/10.  
 DR N-PSDB: Q10867.  
 PT Efficient genetic cloning system - useful for cloning cDNA copies  
 PT of eukaryotic mRNAs of all sizes and for library preparation.  
 PS Disclosure: Fig 9b; 103pp: English.  
 CC The sequence was deduced from a cDNA sequence obt'd. using the  
 CC lambda(pCEV27) expression cloning system of the International cDNA  
 CC transforming cDNA from a fufural induced hepatocellular tumour,  
 CC OT18, from mouse strain B6C3F1. A cDNA library was constructed  
 CC from a secondary transformant of the tumour. The sequence was  
 CC from a transformant. The N-terminal portion appears to be an  
 CC unknown sequence, while the C-terminal region is closely related  
 CC to human B-raf and chicken Emil gene prods. There is only one AA  
 CC difference, at posn. 324 where Gly is replaced by Ala in human  
 CC B-raf. The breakpoint does not disrupt the predicted kinase domain  
 CC of the encoded protein.  
 CC See also R10933.  
 CC Sequence 516 AA:  
 S0  
 Query Match 9.4%; Score 318; DB 3; Length 516;  
 Best Local Similarity 28.2%; Pred. No. 5.07e-18;  
 Matches 72; Conservative 72; Mismatches 91; Indels 20; Gaps 16;  
 DB 219 gtvkakwhg-dvavkmlnvctppqqlqaknevgvirknrlmlng-y-stk-pg 274  
 QY 296 GELNKGWQGDIVVKVVKVPEWSTFKSFENECPKLRFSHNVLFVIGACUSTFIR 324  
 DB 275 laivtqwcgsslyhhilietkfi--chaklkldfdringmdyhrkafkrlr 324  
 QY 295 FLIIHWPYSLYNLHE-GINFWVDS-AYVFALEMAWMAFLHLEFLPRHNLNRS 324  
 DB 331 niflbedtkvkgdglatvksrwsghqeqsluslhwdevarvdkakpysf 324  
 QY 324 SWIIEEDTARIS---MADVNFSEU-C-I-GKMAFA-NVAFALAEFLHLEFLPRHNLNRS 324





PA (2878) GENENTECH INC.  
 BB Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP,  
 BB Wood WI,  
 BB WPI: 95-32030/47.  
 BB N-PSDB: 049754.  
 BB Apolact antibodies which activate specific protein tyrosine  
 BB kinase(s) also activate chimeric proteins of kinase extracellular  
 BB domain and a constant domain, said for studying, and therapeutic  
 BB modulation of cell growth and differentiation  
 BB Disclosure, Page 50-58, 40pp, English.  
 BB DNA probes based on protein tyrosine kinase (PTK) sequences were used  
 BB to screen cDNA libraries to identify novel PTK genes. A first set  
 BB (library) was isolated from lymphocytes and megakaryocytic cell  
 BB libraries. The second set (library) was isolated from the cDNA  
 BB library. The cDNA library was used to design drugs that modulate PTK  
 BB activity. PTK and can be used to design drugs that modulate PTK  
 BB activity. 505 AA.  
 BB Sequence: 505 AA.

Query Match: 9.1%; Score 311; DB 15; Length 505;  
 Best Local Similarity: 26.1%; Pred. No. 2,206-17;  
 Matches: 69; Conservative: 70; Mismatches: 107; Indels: 19; Gaps: 15.

DB 229 Idmsqilqkllsgsgfgwglwntfvaatktkfgg-smdgfdilrcaqirnatlr 285  
 QY 192 IFEKLNELTNENHSGELNKGFWQGN-IVVKLVKVPDMSTRKSPDNCEPRLIFS 246  
 DB 226 hpkilqlyavctldcp-tylitemlraslgerlgnstgskvhltygydaaqvasma 343  
 QY 247 HFNVLFLVLCQSPAPHPHTLITHMWPVGSLYNVTHPSFNFVVDQSAVKFALDMAROMA 306  
 DB 344 Ylesnyihrdlaarvlgemlnkvadfglarfvvdealyesrlkfpvawape 403  
 QY 307 FLHT---LEP-LIPRAL-NRSV-WIDEDMTARISMAVDKFSFQCPGMKAPA-WVAPE 359  
 DB 404 al-rsnkfsiks-dwvsfgillyellytgmypsgmtgaqvgmla-qpyrlpysncp 459  
 QY 360 ALQKKPEDINRPSACWSPAVLLWELT-PEVPPFANISNMEIGMKVALEGLPTIPPSIS 419  
 DB 460 qqfynimlecnwaeptfeti 483  
 QY 419 PHVCKLMKCMEDPAKPRFDMI 442

RESULT 14  
 ID A71132 standard; Protein: 466 AA.  
 AC A71132:  
 DE 27-OCT-1995 (first entry)  
 DE N-terminal truncated cytoplasmic tyrosine kinase.  
 KW cytoplasmic; tyrosine kinase; blood; cell differentiation;  
 KW screening; anticancer agent; SH3; src homology domain.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT domain 7..70  
 FT domain /note= "SH3 domain"  
 FT domain 81..155  
 FT domain /note= "SH2 domain"  
 FT domain 192..438  
 FT domain /note= "tyrosine kinase domain"  
 FN W09506113-A.  
 PD 02-MAP-1995.  
 PF 25-AUG-1994; J01411.  
 PF 25-AUG-1993; JP-210403  
 PF 26-MAP-1994; JP-058553.  
 PA (ASAH) ASAH KASEI KOGYO KK.  
 PI Sakano S.  
 DR WPI: 95-106842/14.  
 DR N-PSDB: 084888.  
 PT Cytoplasmic tyrosine kinase and antibody recognising it - for  
 PT screening chemical substances for tyrosine kinase inhibitory or  
 PT activating activity for use as cancer therapy  
 PS Claim 1; Page 40-42; 58pp; English  
 CC A cytoplasmic tyrosine kinase which has enhanced expression  
 CC connection with blood cell differentiation has been isolated  
 CC human UT-7 blood cell line. This sequence comprises an N-terminal  
 CC truncated fragment of the enzyme (residues 42-507 of R71132).  
 CC sequences and antibodies raised against the enzyme, are useful for  
 CC screening agents for inhibiting or activating activity on the tyrosine  
 CC kinase, for use as anticancer agents.  
 SO Sequence: 466 AA.

Query Match: 9.1%; Score 406; DB 15; Length 466;  
 Best Local Similarity: 28.2%; Pred. No. 6,256-17;  
 Matches: 75; Conservative: 70; Mismatches: 101; Indels: 20; Gaps: 15.

DB 232 lnlqllqllqadlgsgsfavlgqglgllpkyvknkprkz-tylqglactatymtvgq 444  
 QY 194 IFEKLNELTNENHSGELNKGFWQGN-IVVKLVKVPDMSTRKSPDNCEPRLIFS 247







[illegible]

[illegible]

241	VT-PSLVTVSMGIAGMYLH-LKVI-HFD-LKSPNMLIVYGVVYVTSCTGVNLS	
297	FVVDQSQAVKALDVGSMAPLITLELIPPHALNFSVNIIDMTARIS-WADYKFS	
326	QSTKSFAGTIVAKAEPVINEPV-SEK-VD-WKSFQVNLWELTETINYYDTSK	
345	CPGPM-YA-P-ANVAPEALQKKPEDTNPSPADWKSFAVLLWELTVEVPALNS	
354	GWGNSLSLHPVSS-CPDGKILLIPQWNKKPNPSPFQILLHLD 358	
402	KVAIEGLPTIPPGISPHVCK-LMKICMNETPAKPKEDMIVILE 447	
RESULT	11	
ENTRY	JH0559	#type complete
NAME	Protein-tyrosine kinase (EC 2.7.1.12) CSK - human	
ALTERNATE_NAMES	protein-tyrosine kinase c-ys, protein-tyrosine kinase	
ORGANISM	Homo sapiens	
DATE	30-Jun-1992	#sequence_revision 20-Aug-1994
ACCESSIONS	18-Sep-1998	
PEPIDE	JH0559; S38818; S19024; S19025	
AUTHORS	Brauninger, A.; Holtzsch, U.; Strebhardt, K.; Piesbamen-Waigmann, H	
JOURNAL	Gene (1992) 110:205-211	
TITLE	Isolation and characterization of a human gene that encodes a new subclass of protein tyrosine kinases.	
CROSS-REFERENCES	EMBL:92165060	
REFERENCE	JH0559	
AUTHORS	Brauninger, A.; Karn, T.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Oncogene (1993) 8:1365-1369	
TITLE	Characterization of the human CSK locus.	
REFERENCE	S38818	
AUTHORS	Brauninger, A.; Karn, T.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Oncogene (1993) 8:1365-1369	
TITLE	Characterization of the human CSK locus.	
REFERENCE	S38818	
AUTHORS	Partanen, J.; Armstrong, E.; Bergman, M.; Maelvela, T.P.; Hivonen, H.; Huebner, K.; Alitalo, K.	
JOURNAL	Oncogene (1991) 6:2013-2018	
TITLE	c-ys encodes a putative cytoplasmic tyrosine kinase having the conserved tyrosine kinase phosphorylation site (Y416 (src)).	
REFERENCE	S19024	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-Waigmann, H.	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1993) 90:10411-10415	
TITLE	Two additional protein-tyrosine kinases expressed in human lung: fourth member of the fibroblast growth factor receptor family and an intracellular protein-tyrosine kinase.	
REFERENCE	S19025	
AUTHORS	Holtzsch, U.; Brauninger, A.; Strebhardt, K.; Piesbamen-W	







Thu Jan 14 13:43:06 1999

US-08-955-841-2.rpr

Page:

2000-01-14 13:43:06 US-08-955-841-2.rpr  
11/14/99 13:43:06





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06 1523 AAFIPILSKKWEIIQWENFUSRPFYFIIVHLEMD 1964
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07 410 PPIPPGISPVCKMKICMNEPKSPFFEMVIFRMQD 451
      ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
AC AB-DROME STANDARD; FRT. 1520 AA.
AC P0522;
DI 21-JUL-1986 (REL. 01, CREATED)
DI 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
DI 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE TYROSINE-PROTEIN KINASE DASH/ABL (EC 2.7.1.112)
GN DASH OR ABL-1.
OC SCOPHELIA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
PN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE; 8814728.
PA HENKENEYER M.J., BENNETT P.L., GERTLER F.B., HOFFMANN F.M.;
RI MOL CELL BIO; 8:843-853(1988).
RN [2]
RP SEQUENCE OF 374-648 FROM N.A
RX MEDLINE, 84082064.
PA HOFFMANN F.M., FRESCO L.D., HOFFMAN-FALK H., SHILO B.-Z.;
PL CELL 35:393-401(1983).
CC -1- CATALYTIC ACTIVITY. ATP + A PROTEIN TYROSINE = ADP +
    PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION. CYTOPLASMIC.
CC -1- SIMILARITY TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
    DOMAIN. BELONGS TO THE ABL SUBFAMILY
CC -1- SIMILARITY CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY CONTAINS 1 SH3 DOMAIN.
DP ENBL; M19692; G158600; -.
DP ENBL; M19690; G158600; JOINED.
DP ENBL; M19691; G158600; JOINED.
DR EVBL; K01042; G157176; -.
DR FRP; A28128; TVPFA.
DE HSPF; P00519; IAB2.
DE FYBASE; FBG0000017; ABL.
DP POSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CP PF-SITE; PS00109; PROTEIN_KINASE_TYF; 1.
DP POSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DE EF-SITE; PS00001; SH2; 1.
DP POSITE; PS00002; SH3; 1.
RW TRANSFERASE; TYROSINE-PROTEIN KINASE. ATP-BINDING PHOSPHORYLATING
SH2 DOMAIN; SH3 DOMAIN.
FT DOMAIN 204 265 SH3.
FT DOMAIN 271 363 SH2.
FT DOMAIN 388 644 PROTEIN KINASE.
FT NP_BIND 394 402 ATP (BY SIMILIATY).
FT BINDING 417 417 ATP (BY SIMILIATY).
FT ACT_SITE 509 509 RV SIMILIATY
FT MOD_RES 539 539 PHOSPHORYLATION (AUTO-) (BY SIMILIATY)
FT CONFLICT 374 377 LSPF VS ASAC (IN REF 2).
FT CONFLICT 645 648 ESS VS VGVV (IN REF 2).
SV SEQUENCE 1520 AA, 161836 MW, 165337 Da
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Query Match	10.18	Score 340	DB 1	Length 152
Best Local Similarity	30.78	Pred. No. 4,96e-45		
Matches	81	Conservative	53	Misaligning 28
				218 gaps
1	302	KLGGDGEVEAVKNGKNGNTVAKEIF	1	ELTMAKPKETITPMAMKCHWPHENL
2	112	KLNNHSGELKGGW	2	GNELVVVAVNTSTSTSTSTSTSTSTST
3	47	VTFEE PFITTFKXSHNLTLLSAGEL	3	ELAVAVAVAVAVAVAVAVAVAVAVAV
4	256	ALSSPAAPHILITHWKFYSLYWHEGTF	4	NFVVSQVFFALDQAKGMAPET
5	308	PELLAPNLTVDNKLKVAFGFLNEL	5	WFLVTVKALNPETKNTAKNNTV
6	333	PGLFFHALNSGVITDEMTAPIEMAV	6	VFSSFTDPMKAVAVAVAVAVAVAV

NAME	DATE	TIME	LOCATION	REMARKS	STATUS
JOHN DOE	1945	10:00	NEW YORK	ARRIVED	OK
JANE SMITH	1945	11:30	NEW YORK	DEPARTED	OK
ALFRED BROWN	1945	12:00	NEW YORK	ARRIVED	OK
CHARLES WHITE	1945	13:00	NEW YORK	DEPARTED	OK
MARY JONES	1945	14:00	NEW YORK	ARRIVED	OK
ROBERT GARCIA	1945	15:00	NEW YORK	DEPARTED	OK
SUSAN MILLER	1945	16:00	NEW YORK	ARRIVED	OK
THOMAS WILSON	1945	17:00	NEW YORK	DEPARTED	OK
WILLIAM MOORE	1945	18:00	NEW YORK	ARRIVED	OK
YOUNG LEE	1945	19:00	NEW YORK	DEPARTED	OK
ZACHARY HARRIS	1945	20:00	NEW YORK	ARRIVED	OK
ADAM KING	1945	21:00	NEW YORK	DEPARTED	OK
EVELYN SCOTT	1945	22:00	NEW YORK	ARRIVED	OK
FRANK NELSON	1945	23:00	NEW YORK	DEPARTED	OK
GRACE HENDERSON	1945	00:00	NEW YORK	ARRIVED	OK
IRVING PEREZ	1945	01:00	NEW YORK	DEPARTED	OK
JACK ROSS	1945	02:00	NEW YORK	ARRIVED	OK
KAREN COOPER	1945	03:00	NEW YORK	DEPARTED	OK
LARRY BAKER	1945	04:00	NEW YORK	ARRIVED	OK
MICHAEL ADAMS	1945	05:00	NEW YORK	DEPARTED	OK
NANCY HAYES	1945	06:00	NEW YORK	ARRIVED	OK
OSCAR WATSON	1945	07:00	NEW YORK	DEPARTED	OK
PETER FLEMING	1945	08:00	NEW YORK	ARRIVED	OK
QUINN BARNES	1945	09:00	NEW YORK	DEPARTED	OK
RICHARD ROY	1945	10:00	NEW YORK	ARRIVED	OK
SARAH STEVENSON	1945	11:00	NEW YORK	DEPARTED	OK
TIMOTHY GARDNER	1945	12:00	NEW YORK	ARRIVED	OK
URSULA HUGHES	1945	13:00	NEW YORK	DEPARTED	OK
VICTOR CRANE	1945	14:00	NEW YORK	ARRIVED	OK
WALTER HARRIS	1945	15:00	NEW YORK	DEPARTED	OK
XENIA FORD	1945	16:00	NEW YORK	ARRIVED	OK
YVES JONES	1945	17:00	NEW YORK	DEPARTED	OK
ZOE ROSS	1945	18:00	NEW YORK	ARRIVED	OK
ADAM KING	1945	19:00	NEW YORK	DEPARTED	OK
EVELYN SCOTT	1945	20:00	NEW YORK	ARRIVED	OK
FRANK NELSON	1945	21:00	NEW YORK	DEPARTED	OK
GRACE HENDERSON	1945	22:00	NEW YORK	ARRIVED	OK
IRVING PEREZ	1945	23:00	NEW YORK	DEPARTED	OK
JACK ROSS	1945	00:00	NEW YORK	ARRIVED	OK
KAREN COOPER	1945	01:00	NEW YORK	DEPARTED	OK
LARRY BAKER	1945	02:00	NEW YORK	ARRIVED	OK
MICHAEL ADAMS	1945	03:00	NEW YORK	DEPARTED	OK
NANCY HAYES	1945	04:00	NEW YORK	ARRIVED	OK
OSCAR WATSON	1945	05:00	NEW YORK	DEPARTED	OK
PETER FLEMING	1945	06:00	NEW YORK	ARRIVED	OK
QUINN BARNES	1945	07:00	NEW YORK	DEPARTED	OK
RICHARD ROY	1945	08:00	NEW YORK	ARRIVED	OK
SARAH STEVENSON	1945	09:00	NEW YORK	DEPARTED	OK
TIMOTHY GARDNER	1945	10:00	NEW YORK	ARRIVED	OK
URSULA HUGHES	1945	11:00	NEW YORK	DEPARTED	OK
VICTOR CRANE	1945	12:00	NEW YORK	ARRIVED	OK
WALTER HARRIS	1945	13:00	NEW YORK	DEPARTED	OK
XENIA FORD	1945	14:00	NEW YORK	ARRIVED	OK
YVES JONES	1945	15:00	NEW YORK	DEPARTED	OK
ZOE ROSS	1945	16:00	NEW YORK	ARRIVED	OK
ADAM KING	1945	17:00	NEW YORK	DEPARTED	OK
EVELYN SCOTT	1945	18:00	NEW YORK	ARRIVED	OK
FRANK NELSON	1945	19:00	NEW YORK	DEPARTED	OK
GRACE HENDERSON	1945	20:00	NEW YORK	ARRIVED	OK
IRVING PEREZ	1945	21:00	NEW YORK	DEPARTED	OK
JACK ROSS	1945	22:00	NEW YORK	ARRIVED	OK
KAREN COOPER	1945	23:00	NEW YORK	DEPARTED	OK
LARRY BAKER	1945	00:00	NEW YORK	ARRIVED	OK
MICHAEL ADAMS	1945	01:00	NEW YORK	DEPARTED	OK
NANCY HAYES	1945	02:00	NEW YORK	ARRIVED	OK
OSCAR WATSON	1				

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RESULT 7
ID EP33_RAT STANDARD: PR1: 984 AA.
AC 009680:
CD 01-NOV-1997 (REL. 35, CREATED)
DDT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE EPHRIN TYPE-A RECEPTOR 3 PRESEQUENCE (EC 2.7.1.12) (HYDROPHOBIC PHOSPHOLIPASE)
DU KINASE RECEPTOR REK4).
EN EPH3 OR REK4.
LN RATTUS NORVEGICUS (RAT).
OR EPIKARYOTIA: METAZOA: CHORDATA: VERTEBRATA: EPIRAPHIA: MAMMALIA.
OC EUROTHERIA: RODENTIA.
ON [1]
OR SEQUENCE FROM N.A.
AC STRAIN-SPRAGUE-DAWLEY,
CD LI Y. Y., MCTEPHAN C. F., FELDMAN A. M.;
DD SUBMITTED (DEC-1996) TO EMBL/GENBANK/NCBI DATA BANKS.
DE FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS D
DU EPHRIN-A2, -A3, -A4 AND -A5.
EN CATALYTIC ACTIVITY: ATP -> A PROTEIN TYROSINE KINASE.
LN SURCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
OC SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE EPHRIN-A
DU DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
EN SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
AC EMBL_069276: G16987422;
CD PROSITE: PS00107; PROTEIN_KINASE_ATP; 1
DD PROSITE: PS00109; PROTEIN_KINASE_TYR; 1
DE PROSITE: PS00011; PROTEIN_KINASE_DWM; 1
DU PROSITE: PS00790; RECEPTOR_TYR_KIN_V; 1
EN PROSITE: PS00791; RECEPTOR_TYR_KIN_V; 1
LN PROSITE: PS01186; EGF_2; UNKN_WN; 1
OC TRANSFERASE: TYROSINE-PROTEIN KINASE; ATP-BINDING; PHOSPHORYLATION
DU RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
EN SIGNAL 1 20
AC CHAIN 21 984
CD DOMAIN 21 541
DE TRANSMEM 542 565
DU TRANSMEM 566 984
EN DOMAIN 21 321
CD DOMAIN 322 432
DE DOMAIN 433 529
DU DOMAIN 530 883
EN NP_BIND 628 636
CD BINDING 634 654
DE ACT_SITE 747 747
DU MOD_RES 760 780
CD CARBOHYD 212 232
DE CARBOHYD 337 337
DU CARBOHYD 391 391
EN CARBOHYD 404 404
CD CARBOHYD 493 493
DE SEQUENCE 984 AA; 110227 MW; 6042E20F CRC32;

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Query Match 9.5%; Score 321; DB 1; Length 100;  
Best Local Similarity 27.8%; Pred. No. 4, 690-41;  
Matches 67; Conservative 54; Mismatches 93; Indels

265	PTLIITHMPQSGSYNVLHE-GTFVYDQSQAVKFDALDARGMAFHTLEPI	QY
143	RIPLHEDLVKIGDFGLATVKSQMSWSHOFELSSGLMKATEVYKMTKPS	DB
324	SWIMDEDMTAFIS--NADVKFSQ-C-P-GRMYAPA-KVAPEALQKPESTNA	QY
203	REGIVLYELMISQSPYKININFT-LIFMWISLSELSLWNTENFFKPKEMAR	DB
377	FAVLVWELVIREVFFADLSNME-IGNKVALEGLRITP-IGISPHVK-LKA	QY
263	RDERPLFPQILASIE 277	DB
433	PAKRPKEDMIVPILE 447	QY

Search completed: Wed Jan 13 12:13.47 1999  
Job time : 33 secs.

95	VAKLEAV	30118	AFQFQLEAGMGTCHHRTITPQVWYTSFP-VWIVTVMNGS	706	
96		111			
97	VAVALPVA	WTFSTSTPNPQSGRTSTPQPVVLGACSPAPPHRTITHNNPYGS	274		
98		111			
99		111			
100		111			
101	LDLEPRHJALVQ	LAUWKA	QJASQWELKMS	WVEDP-LAERHILNSHLYVQ	762
102		111			
103	LVNVH	EGNIVLVSJAVHNLTPARQAFHTITPTTPHALNSPSWIDRHMIAPI	335		
104		111			
105	SDQSLAVLEDEPAAVT	TROCKTPIVSTFENIAVPKRTISASDWYSGIVLWNVMSG	821		
106		111			
107		111			
108	SVLVVSEPI	TPQRTAKWABEAL	QVPEFTNPP--SA	DKMSFAVLEWELVT-P	388
109		111			
110		111			
111		111			
112	LVKINQSN	LVYLVANVETLEPNSQALVQLEWQKTPNNPKFEQIVSIILK	880		
113		111			
114	LVVPADLSR	HEIKVALLDLEPTTPPISPSHVFKIKICMNEEDPAKPKFDMVIPLEK	448		
115		111			
116		111			
117		111			
118		111			
119		111			
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181		111			
182		111			
183		111			
184		111			

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RESULT 15
AC KRAL-MOUSE
AC STANDARD, PRI: 228 AA.
AC P28028
AC 01-AUG-1992 (REL. 23, CREATED)
AC 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
AC 01-OCT-1992 (REL. 34, LAST ANNOTATION UPDATE)
AC 01-OCT-1992 (REL. 34, LAST SEQUENCE UPDATE)
DE B-KAE PACTO-NUCLEOLAR SEARINE-THREONINE-PROTEIN KINASE (EC 2.7.1.1)
DE (FRAGMENT).
DE BRAF OR B-BRAF.
DE MCS MUSCULUS (MOUSE).
DE EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DE EUTHERIA; RODENTIA.
DE
DE
DE SEQUENCE FROM N.A.
DE MEDLINE: 91271351.
DE MIKI I., FLEMING I.F., GREENE M., MOLLOY C.J., BLAM S.B.,
DE REYNOLDS S.H., AARONSON S.A.;
DE PROC. NATL. ACAD. SCI. U.S.A. 88:5167-5171(1991).
DE FUNCTION INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
DE FROM THE CELL MEMBRANE TO THE NUCLEUS.
DE FUNCTION: KAE PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
DE HIPPOCAMPAL NEURON.
DE SIMILARITY WITH THE CONSERVED CATALYTIC DOMAINS OF SFP/THP-
DE PROTEIN KINASES. BELONGS TO THE MIL/PAF SUBFAMILY.
DE SIMILARITY CONTAINS A COPY OF THE CINC-DEPENDENT PHOSPHO-
DE ESTER AND DAG BINDING DOMAIN.
DE EXML: M04423; CSEESTER; ALI:MIIL.
DE PIR: A40951; TVMSBF.
DE WAD: M3188190; BRAF.
DE PROSITE: P500167; PROTEIN KINASE ATP: 1.
DE PROSITE: P500168; PROTEIN KINASE ST: 1.
DE PROSITE: P500169; PROTEIN KINASE DOM: 1.
DE PROSITE: P500170; DAG-BINDING DOMAIN: PARTIAL.
DE PROSITE: P500171; SEARINE-THREONINE PROTEIN KINASE; ZINC:
DE TRANSFERASE; SEARINE-THREONINE PROTEIN KINASE; PHOTO-OXIDOREDUCTASE; ZINC:
DE ATP-BINDING; PHOSPHO-ESTER BINDING.
DE NON_TER: 1
DE DOMAIN: 19 279 PROTEIN KINASE.
DE BINDING: 25 32 ATP (BY SIMILARITY).
DE BINDING: 45 45 ATP (BY SIMILARITY).
DE ACT_SITE: 138 138 BY SIMILARITY.
DE SEQUENCE 228 AA. SOURCE MW: 25275632 GRC32.

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[illegible]



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321 9.5 954 4 Q10761 MIXED LINEAGE KINASE 2 1.07e-37  
320 9.5 974 13 Q90777 C-EVX PROTO-ONCOGENE P 1.77e-37  
318 9.4 450 13 Q73786 C-SPC KINASE 4.20e-37  
317 9.4 485 5 F49B2.5 2.70e-37  
316 9.4 485 5 VNK-MENDELIUM PROTEIN 5.87e-37  
315 9.4 511 11 Q64103 RECEPTOR-PROTEIN KINOS 1.17e-36  
314 9.4 975 11 Q60633 GAG-EMILIN POLYPEPT 4.27e-36  
313 9.4 1079 14 Q65614 LEUCINE ZIPPER BEARING 2.77e-36  
312 9.3 966 4 Q42833 TYROSINE KINASE 3.77e-36  
311 9.3 1382 13 Q90375 TYROSINE KINASE 1.09e-35  
310 9.2 588 5 Q45032 SRC-RELATED INTESTINAL 1.08e-35  
309 9.1 451 11 Q64434 ACTIVATED MET-ONCOGENE 2.58e-35  
308 9.0 455 4 Q12875 IGF-1R FUSION PROTEIN 1.56e-35  
307 9.0 523 4 Q13080 CELLULAR PROTO-ONCOGEN 1.77e-35  
306 9.0 999 4 Q12866 HEPATOCYTE GROWTH FACT 2.58e-35  
305 9.0 1382 11 P97579 TYROSINE KINASE C1K7 K 2.64e-35  
304 8.9 490 13 Q07495 C24A1.3 PROTEIN 2.64e-35  
303 8.9 842 5 Q17055 PROTO-ONCOGENE TYROSIN 5.70e-35  
302 8.9 981 14 Q19477 P10-ONCOGENE TYROSIN 6.97e-35  
301 8.9 1130 4 Q13843 SRC-RELATED TYROSINE K 6.97e-35  
300 8.8 506 11 Q62862 PKF1 PROTEIN (FRAGMENT 4.37e-34  
299 8.7 204 10 Q39756 TAK1 4.37e-34  
298 8.7 616 13 Q73613 AXL-RELATED RECEPTOR 2.58e-34  
297 8.7 873 13 Q98949 EPH-LIKE RECEPTOR TYR 4.37e-34  
296 8.7 993 13 Q42422

# ALIGNMENTS

RESULT 1 PRELIMINARY: PRI: 452 AA.  
ID Q13418  
AC Q13418:  
DI 01-NOV-1996 (TREMBLREL\_01, CREATED)  
DI 01-AUG-1998 (TREMBLREL\_07, LAST SEQUENCE UPDATE)  
DI 01-AUG-1998 (TREMBLREL\_07, LAST ANNOTATION UPDATE)  
DE INTEGRIN-LINKED KINASE.  
GN ILK.  
OS HOMO SAPIENS (HUMAN).  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE: 96135142.  
RA HANNIGAN G.E., LEUNG-HAGSTEIJN C., FIIZ-GIBSON L., COPPIN N.  
PA PACEVA G., FILMS J., BELL J.C., DEDHAR S.:  
PI NATURE 379:91-96(1996)  
PN [2]  
RP SEQUENCE FROM N.A.  
PA DEDHAR S., HANNIGAN G.E.:  
PI SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [3]  
PP SEQUENCE FROM N.A.  
RA DEDHAR S., HANNIGAN G.E.:  
PI SUBMITTED (MAY-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
CP EMBL:140282; GENBANK:U00002;  
YW INDEPIN.  
SQ SEQUENCE 452 AA; 51419 MW; 76289FF2 CRC32;

Query Match 100.0%; Score 3377; DB 4; Length 452;  
Best/Local Similarity 100.0%; Pred. NO. 0.00e+00;  
Matches 452; Conservative 0; Mismatches 0; Gaps 0  
DE 1 MDIETQCRGNAVAVPLWLDNTENDLNGDGHGSPHLWACRGSAVAVV  
QY 1 MDIETQCRGNAVAVPLWLDNTENDLNGDGHGSPHLWACRGSAVAVV  
DB 61 NVNFGDDTFLHAAASHGRDIVQKLLQYKADINAVNHNHGVNPLHYAGNVA  
QY 61 NVNFGDDTFLHAAASHGRDIVQKLLQYKADINAVNHNHGVNPLHYAGNVA  
DB 121 ANCALYSICKYGEVDPVKAKAPPELLPEPAKFMQNLNRPYKDTIKGTRFNS  
QY 121 ANCALYSICKYGEVDPVKAKAPPELLPEPAKFMQNLNRPYKDTIKGTRFNS

DB 421 VKLIMKICMNEOPAKPKPFDMIVT::FRMGGA 452  
 422 |||||||||||||||||||||||||  
 QY 421 VKLIMKICMNEOPAKPKPFDMIVPIERKMQIK 472  
 422 |||||||||||||||||||||||||

RESULT 3  
 ID 065833  
 AC 065833  
 DT 01-AUG-1998 (TPEMBLREL 07, GRALETA)  
 DI 01-AUG-1998 (IREMBREL 07, LAST SEQUENCE UPDATE)  
 DT 01-AUG-1998 (TREMBREL 07, LAST SEQUENCE UPDATE)  
 DE TCT2 PROTEIN.  
 GN TCT2.  
 OS LYCOPERSICON ESCULENTUM (TOMATO).  
 OC FRUITARIA; PLANTA; EUPHYCOPHYTA; ANGIOSPERMAE; DIPSACALES.  
 OC SOLANALES; SOLANACEAE.  
 RN (1)  
 RP SEQUENCE FROM

STRAIN=CV. AILSA CRAIG;  
 LIN 2: HACKETT R.M., PAYTON S., GRIFPES N.D.;  
 SUBMITTER (MAP:1998) TO: EMIL GINSAPPE, DORT DATA BANKS.  
 ENBL: AJ005077; E1296723; ...  
 PROTEIN KINASE.  
 NO SEQUENCE 981 AA; 107175 MW; C02DB613 CR42;  
 Query Match 13.6%; Score 459; DR 100; Local 941;  
 Best Local Similarity 32.9%; Evid. NO. 3; 400-469;  
 Matches 81; Conservative 66; Mismatches 43; Labels 11; Gaps  
 b 712 GEVYHADWNGTVEAVKKFLDDFSAALAFKPKVPIHPSRIRKVVVDFGALFPIH  
 y 205 GRMGRKBPWGNDIVVKVLRKDWSTKSPGPNFVPSFPIPIHNAIVLVASLPAH  
 b 770 LSLTEFLPRGLPIIHP-PRFQVPPPTPTALAKRMCHHSHSNPTLVHPSKSN  
 y 265 PLTIHWPYGLSVNLVHEGTFNVFVDSQAVFPAIMARGRAPIHLEPIHFAHNS  
 b 829 LIVITDNNVKKVDFGLSKLKHNTFLSSKNSIAGTPIKVVAVPVLN...

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345 VUID-E-DMTA-RISMADVAF-SQCPGPMY-AFAWVAFAIUKKIDGNDZAFMUSVA 00
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
886 VILNELATLRPLWCSGMPNDQMVGVGFQNKLEIFKELDFIVAFIUKKIDGNDZAF 00
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
380 VLLWEIVTVEPPFADUSNMEIGMKVALEGNLRTIINISGVTSLANKIDUNHFAKFK 00
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
945 AOLIVALTPLO 956
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
440 DMIVPILEKML 450
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

SUBMIT 4 PRELIMINARY: PFI: 829 AA.
024027:
024027:
01-JAN-1998 (TREMBLEL 05, CREATED)
01-JAN-1998 (TREMBLEL 05, LAST SEQUENCE CHANGE)
01-JUN-1998 (TREMBLEL 06, LAST ANNOTATION RELEASE)
HYPOTHEICAL 94.9 KD PROTEIN.
LYCOPERSICON ESCULENTUM (TOMATO).
FUKARYOTA; PLANTA, EMBRYOPHYTA; ANGIOSPERMAE; Dicotyledoneae.
SOLANALES; SOLANACEAE.
[1]
SEQUENCE FROM N.A.
STRAIN-UC82B;
WANG Y., LI N.;
PLANT PHYSIOL 114:1135-1135(1997).
EMBL: Y13273, E334294; -
PROSITE PS00106; PROTEIN_KINASE_ST_1.
PFAM: PF00069; PKINASE.
HYPOTHEICAL PROTEIN; PROTEIN KINASE.
SEQUENCE 829 AA: 91912 MW, K50619CF (06/92);

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11 443 LHSQVAVVERGAGSFANVSLGINKVYKVAIKLK-NE-SISNDEKIKVNSLKHSH 193
12 1110 PNVVTFMGA-KI--DP-PCIFTEYLOGSLYLVH-CKIPVNTGKRRKCH 248
13 188 IDFKQLNFLTILKNEHSGELWGRWCNNIVVVKLVKVDWSTPKSPKINIE 274
14 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
15 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
16 257 DONTVCVADFGSLSKKIYSGDYRQGRKAKMPVKWIA:PSIADRVY-ISK 274
17 329 EDMTARIS-MA-DVK-FS--FOCEGRMY-APA-WVADEPAI:CKPETHRRKADPK 274
18 314 MWEITTRGMTYPPGVQNHEN-YDVLHGHRIKOPEDLDELFDYDMSWAAK 274
19 382 LWELVTREV-PAADLSNMEIGMKVALEHETPHALNSP 274
20 373 VLRLOLEKLS 393
21 444 LHSQVAVVERGAGSFANVSLGINKVYKVAIKLK-NE-SISNDEKIKVNSLKHSH 193
22 1110 PNVVTFMGA-KI--DP-PCIFTEYLOGSLYLVH-CKIPVNTGKRRKCH 248
23 188 IDFKQLNFLTILKNEHSGELWGRWCNNIVVVKLVKVDWSTPKSPKINIE 274
24 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
25 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
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28 314 MWEITTRGMTYPPGVQNHEN-YDVLHGHRIKOPEDLDELFDYDMSWAAK 274
29 382 LWELVTREV-PAADLSNMEIGMKVALEHETPHALNSP 274
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32 1110 PNVVTFMGA-KI--DP-PCIFTEYLOGSLYLVH-CKIPVNTGKRRKCH 248
33 188 IDFKQLNFLTILKNEHSGELWGRWCNNIVVVKLVKVDWSTPKSPKINIE 274
34 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
35 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
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40 373 VLRLOLEKLS 393
41 446 LHSQVAVVERGAGSFANVSLGINKVYKVAIKLK-NE-SISNDEKIKVNSLKHSH 193
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49 382 LWELVTREV-PAADLSNMEIGMKVALEHETPHALNSP 274
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52 1110 PNVVTFMGA-KI--DP-PCIFTEYLOGSLYLVH-CKIPVNTGKRRKCH 248
53 188 IDFKQLNFLTILKNEHSGELWGRWCNNIVVVKLVKVDWSTPKSPKINIE 274
54 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
55 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
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75 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
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83 188 IDFKQLNFLTILKNEHSGELWGRWCNNIVVVKLVKVDWSTPKSPKINIE 274
84 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
85 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
86 257 DONTVCVADFGSLSKKIYSGDYRQGRKAKMPVKWIA:PSIADRVY-ISK 274
87 329 EDMTARIS-MA-DVK-FS--FOCEGRMY-APA-WVADEPAI:CKPETHRRKADPK 274
88 314 MWEITTRGMTYPPGVQNHEN-YDVLHGHRIKOPEDLDELFDYDMSWAAK 274
89 382 LWELVTREV-PAADLSNMEIGMKVALEHETPHALNSP 274
90 373 VLRLOLEKLS 393
91 451 LHSQVAVVERGAGSFANVSLGINKVYKVAIKLK-NE-SISNDEKIKVNSLKHSH 193
92 1110 PNVVTFMGA-KI--DP-PCIFTEYLOGSLYLVH-CKIPVNTGKRRKCH 248
93 188 IDFKQLNFLTILKNEHSGELWGRWCNNIVVVKLVKVDWSTPKSPKINIE 274
94 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
95 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
96 257 DONTVCVADFGSLSKKIYSGDYRQGRKAKMPVKWIA:PSIADRVY-ISK 274
97 329 EDMTARIS-MA-DVK-FS--FOCEGRMY-APA-WVADEPAI:CKPETHRRKADPK 274
98 314 MWEITTRGMTYPPGVQNHEN-YDVLHGHRIKOPEDLDELFDYDMSWAAK 274
99 382 LWELVTREV-PAADLSNMEIGMKVALEHETPHALNSP 274
100 373 VLRLOLEKLS 393

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RESULT 10
ID 062194 PRELIMINARY: PRI: 511 AA.
AC 062194:
DI 01-NOV-1996 (TREMBLREL, 01, CREATED)
DI 01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DI 01-JUN-1998 (TREMBLREL, 06, LAST ANNOTATION UPDATE)
DE RECEPTOR PROTEIN-TYROSINE KINASE (FRAGMENT)
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TEIARAP; EUMETAZOA
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CD-1; TISSUE-TESTIS
RA DOWDS C.A.; BURKS D.J.; SALING P.M.
RL SUBMITTED (JAN-1996); TO EMBL, GENE BANK, JGI DATA BANKS.
LK EMBL, L11625; G1161126;
DR PFAM; PF00069; pkinase.
KW TYROSINE-PROTEIN KINASE.
FT NON_TER
SQ SEQUENCE 511 AA; 57410 MW; 40110 AA; 36042;

Query Match
Best Local Similarity 9.98; Score 446; DB 11; Length 1448;
Matches 77; Conservative 62; Mismatches 66; Indels 243; Gaps 199
Db 140 VAVTKMLNFSORETEEFELSEAACHKDNHNUNVILGCVCTEESQVTPKRMVILPTMK 199
QY 217 IVVKLVKVRDWSTRKSRDFNECPRLRIFSHNVLPLVGLAC-Q-SIDA PHETLTHMP 274
Db 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
QY 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
Db 257 DONTVCVADFGSLSKKIYSGDYRQGRKAKMPVKWIA:PSIADRVY-ISK 274
QY 329 EDMTARIS-MA-DVK-FS--FOCEGRMY-APA-WVADEPAI:CKPETHRRKADPK 274
Db 314 MWEITTRGMTYPPGVQNHEN-YDVLHGHRIKOPEDLDELFDYDMSWAAK 274
QY 382 LWELVTREV-PAADLSNMEIGMKVALEHETPHALNSP 274
Db 373 VLRLOLEKLS 393

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RESULT 10
ID 062194 PRELIMINARY: PRI: 511 AA.
AC 062194:
DI 01-NOV-1996 (TREMBLREL, 01, CREATED)
DI 01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DI 01-JUN-1998 (TREMBLREL, 06, LAST ANNOTATION UPDATE)
DE RECEPTOR PROTEIN-TYROSINE KINASE (FRAGMENT)
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TEIARAP; EUMETAZOA
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CD-1; TISSUE-TESTIS
RA DOWDS C.A.; BURKS D.J.; SALING P.M.
RL SUBMITTED (JAN-1996); TO EMBL, GENE BANK, JGI DATA BANKS.
LK EMBL, L11625; G1161126;
DR PFAM; PF00069; pkinase.
KW TYROSINE-PROTEIN KINASE.
FT NON_TER
SQ SEQUENCE 511 AA; 57410 MW; 40110 AA; 36042;

Query Match
Best Local Similarity 9.98; Score 446; DB 11; Length 1448;
Matches 77; Conservative 62; Mismatches 66; Indels 243; Gaps 199
Db 140 VAVTKMLNFSORETEEFELSEAACHKDNHNUNVILGCVCTEESQVTPKRMVILPTMK 199
QY 217 IVVKLVKVRDWSTRKSRDFNECPRLRIFSHNVLPLVGLAC-Q-SIDA PHETLTHMP 274
Db 200 YGDLHTFLLYSLRNTGPKYIHLQTL-LKFMPIADIMYELNSRN-ETEDP 274
QY 274 YG---S--LYNVLHEGTFNVVDSQAVKALIMKGMALHTLEHETPHALNSP 274
Db 257 DONTVCVADFGSLSKKIYSGDYRQGRKAKMPVKWIA:PSIADRVY-ISK 274
QY 329 EDMTARIS-MA-DVK-FS--FOCEGRMY-APA-WVADEPAI:CKPETHRRKADPK 274
Db 314 MWEITTRGMTYPPGVQNHEN-YDVLHGHRIKOPEDLDELFDYDMSWAAK 274
QY 382 LWELVTREV-PAADLSNMEIGMKVALEHETPHALNSP 274
Db 373 VLRLOLEKLS 393

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[illegible]

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04-APR-1994; US-222616.
PA (GENIE) GENENTECH INC.
PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
PT Wood WI;
DR WPI: 95-366160/47.
DP N-PDB: T030q7.
PT Agonist antibodies which activate specific protein tyrosine
kinase(s), also activate chimeric proteins of kinase extracellular
domain and Ig constant domain, useful for studying, and therapeutic
modulation of, cell growth and differentiation
PS Disclosure: Page 56-58; 125pp; English.
CC DNA probes based on protein tyrosine-kinase (PTK) sequences were used
to screen cDNA libraries to identify novel PTK genes. A LIPK2 gene
(703207) was isolated from lymphocytic and megakaryocytic cell
libraries. The encoded novel PTK, LIPK2 (P85829), shows homology to
known PTKs, and can be used to design drugs that modulate PTK
activity.
SQ Sequence 505 AA;
Query Match 55.3%; Score 1074; DB 15; Length 505;
Best Local Similarity 54.2%; Pred No 6, 375-90;
Matches 141; Conservative 56; Mismatches 59; Indels 4; Gaps
L1 222 LIRSLILKLGSGGFFERWELKADITFVATLLIGTSSTDTTIDQIIMTIIIVY 249
C1 1TPESLRLEVVLGGCFGEVVMGTWNGIKVAIKLKSTETWPLAFLSEAIMKKRIKCK 27
D1 269 LIQIRAVCTIEDPYIFTELARHSLIQGLCDTSKILLIPIIDHAASVASDAVLESR 348
Q1 51 LVPLFAVVS-EPIVIIVTEFTMGSLDFLRKEGSKFKLPQLVTNACIALAGAYIERM 119
D1 349 RYIHRLDAARNLVGETALYKVADFGIARVFVDSDIOYOSTHEIKPKVKTPEAIRSH 419
Q1 120 NVIHPDLAAINTVGDNLVCKIADSGIAPL--IERNE-VTAPOCAKFEPKMTAPEALYS 179
D1 409 KSIKSDWSFGILLYEITYGKMPSYGNTGAQVLMIAQYRIQPSCPCPGFINITE 199
Q1 177 FTIIRSDVMSFOILLTEIVTFGVFPVPVKNVPEVLEVEFSIPMPFGCPERSIEIKYA 249
D1 459 CWNAEKPKEPTFTETIRWKLE 488
Q1 237 CWVKPFDEPPTTEYICSFLE 256
RESULT 6
ID R41941 standard; Protein: 505 AA.
AC R41941;
DE 10-MAR-1994 (first entry)
KW PTK gene LPTK-2 prod
KW PTK, protein tyrosine kinase; catalytic domain; cavity; mutation
KW lymphocyte; amplification; primer; polymerase chain reaction
KW Homo sapiens.
PN WO9315201-A.
PD 05-AUG-1993.
PE 22-JAN-1993; US-826935.
PP 22-JAN-1993; US-826935.
PR (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
PI Arndham H, Cowley S, Groopman J, Scadden D;
DR WPI: 93-320330/40.
DP N-PDB: Q49754.
PT New protein tyrosine kinase genes and proteins encoded by genes
are of human mega-karyocytic origin
PS Claim 3; Fig 5; 60pp; English.
CC PTK genes were identified using two sets of degenerative
oligonucleotide primers: a first set which amplifies all PTK DNA
segments (Q49743-44), and a second set which amplifies highly
conserved sequences present in the catalytic domain of the PTK
subclass of PTKs (Q49745-46). The PTK genes identified are described
in Q49747-57 and Q41897-02.
CC The PTKs are expressed in lymphocytic cells, as well as
megakaryocytic cells, the partial and full-length LIPK2 gene
sequences are given in Q49749 and Q49754 respectively. The
protein sequence corresp. to Q49749 is termed (claim 7) and

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181 KATWAGSAGGKLVKADGVNLYNMYWVRLVAVETWTFPFGGFESEHEDLFLWKR 240
489 spadipefaethuf 503
241 DPQERPIE-LYLOSF 254

RESULT
ID P60009 standard: Protein, 254 AA.
AC P60009
DE 12-SEP-1992 (first entry)
DE Sequence of oncogene arg.
DE Therapy: diagnosis; insulin.
KW EP 123727A.
PD 27-AUG-1985.
PR 12-FEB-1986; 300894.
PR 12-FEB-1986; 3070772.
PA (GEN) GENENTECH INC.
PI BOLL CE, GILLICH A, Ramachandran J.
DR M11 55 220367/35.
REX DNA encoding insulin receptor or its fragments - used for
PT synthesis of receptor and mutants for therapeutic and diagnostic
PT use.
EX: Example: Fig 5: 6pp; English.
CC A mutant IR is claimed which may have a mutated alpha-chain, esp. at
CC the precursor processing site. The beta-chain may be mutated, e.g.
CC by deletion of the transmembrane sequence, the tyrosine kinase
CC activity may be inactivated. Fig. 5 is a comparison of sequence and
CC human EGF receptor sequences with that of HIR in the cytoplasmic
CC domain of the insulin receptor beta subunit.
CC Sequence 254 AA.

Query Match 49.0%; Score 942; DB 2; Length 254;
Best Local Similarity 50.5%; Pred. No. 316e-77;
Matches 100; Conservative 99; Mismatches 61; Indels 9; Gaps 9;

Db 1 10qqlldafktrngprlrlflglvdmpr-qkafkikxtapeaalyyftlkdsqsf 60
QY 12 LQSSGIDGVNLSKNGTKVAIKILKIPGIMMPEAFIQACIMKXLRH 70
Db 61 hrdlrakllldkllkkaifakllaklledvrtargaklvglyavuscepfvrlvrym 120
QY 71 EPIIVVTEPTMGKSLDPLKEGEGKEL-KLPVIVNMAQIACDMVIEKMH 127
Db 121 8kgallldfkltrngprlrlflglvdmpr-qkafkikxtapeaalyyftlkdsqsf 176
QY 122 AANIVNENLVRIADQTEAFITFNVTAPQGAFFPIKWTAPPAALVGPFTIKSD 187
Db 177 glltelldktrngprngprngprngprngprngprngprngprngprngprngprng 236
QY 186 GILLIELVTEPTMGKSLDPLKEGEGKEL-KLPVIVNMAQIACDMVIEKMH 247
Db 237 lnylqagll 244
QY 246 ERPTF 248

RESULT
ID R94538 standard: Protein, 441 AA.
AC R94538
DE 12-SEP-1996 (first entry)
DE Description: Abelson tyrosine kinase.
DE Cytoplasmic tyrosine kinase; BMX; haematopoietic cell
DE cell growth, cell proliferation, tumour, diagnosis; therapy.
KW Src280.
PR 12-SEP-1996.
PR 12-SEP-1996; 559029.
PA (USSH) NAI INST OF HEALTH.
PI Krush G, Arronsen SA, King GP.
DR N-PSDB; Q14937.
REX human gene related to abl proto-oncogene - designated
PT "Abelson Related Gene", arg, useful for tumour diagnosis and
PT therapy.
PS Disclosure: Fig 5D: 40pp; English.
CC The human gene encoding this protein is closely related to but
CC distinct from the abl proto-oncogene and is a member of the tyrosine
CC kinase encoding family of genes. Arg is expressed as two transcripts.
CC By analogy with c-abl, the alternative 5' arg sequences have been
CC designated A (Q14936) and B and it is assumed that they are joined
CC to the arg second exon.
CC The amino acid sequence is represented as found in the specification.

```

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PI binding_site /label= Tyrosine-kinase_domain
PI 187...109
PI /label= ATP-binding_region
PI modified_site 332
PI /label= Autophosphorylation_site
PD W09611275-A1.
PD 18-APR-1996.
PR 09-OCT-1995; F10555.
PR 07-OCT-1994; US-320432.
PA (CYHE-) UNIV HELSINKI LICENSING LTD OY.
PI Allitalo K.
DR WPI: 96-209856/21.
REX cytoplasmic tyrosine kinase BMX and related DNA - useful to
PT stimulate haematopoietic cell growth.
PT Disclosure: Page 28-29; 40pp; English.
CC the amino acid sequence (P94538) of tyrosophila Src280 tyrosine
CC kinase was compared with the sequences of 3 members of a
CC newly identified non-receptor tyrosine kinase family, BMX (R94534),
CC IKK (P94535) and TEC (P94536), and with novel human cytoplasmic
CC tyrosine kinase BMX (see also P94533). Close homology was found.
CC Sequence 441 AA;

Query Match 48.0%; Score 933; DB 17; Length 441;
Best Local Similarity 48.6%; Pred. No. 2.58e-76;
Matches 119; Conservative 54; Mismatches 70; Indels 10;

Db 181 lmlmeelsgsgfvrrgkwrsgldavkmkkgstmscdffiesvmtkkgql 120
QY 6 LPFLVKLQGGFGEVMGIMNGITKVAIKILKIPGIMMPEAFIQACIMKXLRH 127
Db 241 grctkhrilvityemkbgslmvlrtbkekalgmgllmqcvguskmvlylerh 187
QY 66 AVVSEB-PYIVVTEPTMGKSLDPLKEGEGKEL-KLPVIVNMAQIACDMVIEKMH 197
Db 301 rilaarndvnsenwkvadfglarylllytssrrtkafktrngprngprngprngprng 360
QY 124 PLPAANTLVGDNLVCKIADQTEAFITFNVTAPQGAFFPIKWTAPPAALVGPFTIKSD 187
Db 361 wrygylmwcifctckmrygriktemvrvgrcilskpkyacokelvdymkklwshape 420
QY 184 VNSPGLITELVTKRGVFPFGVKNPEVLEVEP3VEM-CP-33FESHELKSLTWFEFD 243
Db 421 erpaf 425
QY 244 ERPTF 248

RESULT
ID R15157 standard: Protein, 1182 AA.
AC R15157
DE 12-FEB-1992 (first entry)
DE Abelson Related Gene, B transcript.
DE Arg; diagnosis; therapy; tumour; abl proto-oncogene.
KW Homo sapiens.
OS Homo sapiens.
PN US7559029-A.
PR 22-OCT-1991.
PR 22-OCT-1991.
PR 30-JUL-1990; US-559029.
PA (USSH) NAI INST OF HEALTH.
PI Krush G, Arronsen SA, King GP.
DR N-PSDB; Q14937.
REX human gene related to abl proto-oncogene - designated
PT "Abelson Related Gene", arg, useful for tumour diagnosis and
PT therapy.
PS Disclosure: Fig 5D: 40pp; English.
CC The human gene encoding this protein is closely related to but
CC distinct from the abl proto-oncogene and is a member of the tyrosine
CC kinase encoding family of genes. Arg is expressed as two transcripts.
CC By analogy with c-abl, the alternative 5' arg sequences have been
CC designated A (Q14936) and B and it is assumed that they are joined
CC to the arg second exon.
CC The amino acid sequence is represented as found in the specification.

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Thu Jan 14 13:43:20 1999

US-08-955-841-4.rag

Page

192 192 SOWSEGHILLFELVTKGRVPGWVNEVLEOVERGFRMPCPOSPESLHKLCKWKO 241  
193 193 POKRPTIQQILSSLO 667  
194 194 IIII IIII  
195 195 FORBTFEYIOSPIE 256

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Run time : 47 secs.



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#avian protein kinase homology #label KIN
#binding site phosphorylation #status predicted
#binding site myristated amino end (SH) (in mature
form) #status predicted
#binding site palmitate (Cys) (covalent) #status
predicted
#active site lys #status predicted
#binding site phosphate (Tyr) (covalent) #status
predicted
#binding site phosphate (Tyr) (covalent) #status
predicted
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Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16 27 IPRESLRLEVKLGQCGFGEVWMSSTINIIKVA...LEKIMHSEALIEAGIMKKLHKK 329
17 1 IPRESLRLEVKLGQCGFGEVWMSSTINIIKVA...LEKIMHSEALIEAGIMKKLHKK 329
18 134 LVPYAVVSEPIIYIVTEMTKSGSLIDFKPQPMELKALPQVGMMAAIAIPMAIIPMA 389
19 1 LVPYAVVSEPIIYIVTEMTKSGSLIDFKPQPMELKALPQVGMMAAIAIPMAIIPMA 389
20 61 LVPYAVVSEPIIYIVTEMTKSGSLIDFKPQPMELKALPQVGMMAAIAIPMAIIPMA 389
21 382 YIHRDLRAANILVCGNLVCKTADFNIAHLEFNEVYARQAKH...IAKATIAFAA... 449
22 121 YIHRDLRAANILVCGNLVCKTADFNIAHLEFNEVYARQAKH...IAKATIAFAA... 449
23 442 KSDVMSFGILLTELVTGKVPYPMVNRVLEVERGRMPLQVGFESLHLEH... 509
24 191 KSDVMSFGILLTELVTGKVPYPMVNRVLEVERGRMPLQVGFESLHLEH... 509
25 502 DPDERPTFEYIOSFLE 517
26 241 DPDERPTFEYIOSFLE 256
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virus Y93
#organism Avian sarcoma virus Y93
#accession F01921
#molecule_type mRNA
#cross-references GB:M15990; NID:0181267; PDB:01W1267
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#gene GDB:Y93
#cross-references GDB:119637; OMIM:164890
#map_position 18p11.31-18p11.22
FUNCTION
#description catalyzes the phosphorylation of a tyrosine residue
by ATP
CLASSIFICATION
#superfamily Protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
KEYWORDS
ATP; autophosphorylation; blocked amino end; lipoprotein;
myristylation; phosphoprotein; phosphotransferase;
proto-oncogene; thioester bond; transforming protein;
tyrosine-specific protein kinase
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2-543
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form) #status predicted
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predicted
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predicted
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predicted

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#binding site phosphorylation #status predicted
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predicted
#active site lys #status predicted
#binding site phosphate (Tyr) (covalent) #status
predicted
#binding site phosphate (Tyr) (covalent) #status
predicted
#length 54; #molecular-weight 60792 #checksum 4288
SUMMARY
Query Match 100.0% Score 1943; DB 1; Length 541;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16 27 IPRESLRLEVKLGQCGFGEVWMSSTINIIKVA...LEKIMHSEALIEAGIMKKLHKK 329
17 1 IPRESLRLEVKLGQCGFGEVWMSSTINIIKVA...LEKIMHSEALIEAGIMKKLHKK 329
18 134 LVPYAVVSEPIIYIVTEMTKSGSLIDFKPQPMELKALPQVGMMAAIAIPMAIIPMA 389
19 1 LVPYAVVSEPIIYIVTEMTKSGSLIDFKPQPMELKALPQVGMMAAIAIPMAIIPMA 389
20 61 LVPYAVVSEPIIYIVTEMTKSGSLIDFKPQPMELKALPQVGMMAAIAIPMAIIPMA 389
21 382 YIHRDLRAANILVCGNLVCKTADFNIAHLEFNEVYARQAKH...IAKATIAFAA... 449
22 121 YIHRDLRAANILVCGNLVCKTADFNIAHLEFNEVYARQAKH...IAKATIAFAA... 449
23 442 KSDVMSFGILLTELVTGKVPYPMVNRVLEVERGRMPLQVGFESLHLEH... 509
24 191 KSDVMSFGILLTELVTGKVPYPMVNRVLEVERGRMPLQVGFESLHLEH... 509
25 502 DPDERPTFEYIOSFLE 517
26 241 DPDERPTFEYIOSFLE 256
RESULT 3
ENTRY TVW09
TITLE Protein-tyrosine kinase (EC 2.7.1.12) ysc-1 avian sarcoma
virus Y93
#organism Avian sarcoma virus Y93
#accession F01921
#molecule_type mRNA
#cross-references GB:M15990; NID:0181267; PDB:01W1267
GENETICS
#gene GDB:Y93
#cross-references GDB:119637; OMIM:164890
#map_position 18p11.31-18p11.22
FUNCTION
#description catalyzes the phosphorylation of a tyrosine residue
by ATP
CLASSIFICATION
#superfamily Protein-tyrosine kinase src; protein kinase
homology; SH2 homology; SH3 homology
KEYWORDS
ATP; autophosphorylation; blocked amino end; lipoprotein;
myristylation; phosphoprotein; phosphotransferase;
proto-oncogene; thioester bond; transforming protein;
tyrosine-specific protein kinase
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2-543
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predicted

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#authors
#journal
#title
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##residues 98-145 ##label PYF
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##molecule_type mRNA
##residues 98-117:124-145 ##label PYZ
REFERENCE
#authors Anderson, S.K.; Gibbs, C.P.; Tanaka, A.; Kato, H.;
#journal Mol. Cell. Biol. 1995; 15:123-129
#title Human cellular src gene: Nucleotide sequence and deduced
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##molecule_type mRNA
##residues 192-542 ##label AND
#cross-references GB:X02647; NIDB46588; PIDB00047; PIR01848
REFERENCE
#accession A28832
#authors Parker, P.C.; Mardon, G.; Leber, P.V.; Vignas, B.E.; Rist,
#journal Mol. Cell. Biol. 1985; 5:843-848
#title Isolation of duplicated human c-src genes located on
#accession A28932
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REFERENCE
#accession A34704
#authors Pyper, J.M.; Bolen, J.B.
#journal Mol. Cell. Biol. 1990; 10:2045-2046
#title Identification of a novel neuronal c-Src RNA expressed
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##molecule_type mRNA
##residues 118-123 ##label PY3
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336	Ikawa, S.; Hagino-Yamagishi, K.; Kawai, S.; Yamamoto, T.
353	Toyochima, K.
370	Mol. Cell. Biol. (1989) 9:2420-2429
387	Activation of the cellular src gene by transducing
404	retrovirus.
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591	myristylation phosphoprotein phosphotransferase:
608	transforming protein; tyrosine-specific protein kinase
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676	autophosphorylation) #status predicted
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## SUMMARIES

Result	Query
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303 303 ATP (BY SIMILARITY).
394 BY SIMILARITY.
ACT_SITE 394 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
424 424 V > I (IN RES 23).
372 372 MISSING IN RES 23.
374 390 MISSING IN RES 23.
SEQUENCE 541 AA: 60630 MW: 61609.95 KDa. Length 541.

Query Match: 98.6%, Score 145, IP ID Length 541.
Best Local Similarity 97.3%, Pred. No. 0.00e+00.
Matches 249: Conservative 6; Mismatches 1; Indels 0; Gaps 0.

Db 370 1PESLRLEVLKLGQCGFEVWVGWNGIIIVAKILKILSGEMEARLALGAWYFIDV 324
1 1PESLRLEVLKLGQCGFEVWVGWNGIIIVAKILKILSGEMEARLALGAWYFIDV 324
QY .....

Db 330 LVPLVAVWSEELIVITFMSKGSIDLPKFGDGKYLKLPOLVEMAAALAGCHAYTEEN 419
LVPLVAVWSEELIVITFMSKGSIDLPKFGDGKYLKLPOLVEMAAALAGCHAYTEEN 419
QY .....

Db 61 LVPLVAVWSEELIVITFMSKGSIDLPKFGDGKYLKLPOLVEMAAALAGCHAYTEEN 419
LVPLVAVWSEELIVITFMSKGSIDLPKFGDGKYLKLPOLVEMAAALAGCHAYTEEN 419
QY .....

Db 390 YIHPDLRAANLLVGNELCKIAEFLALITFNTAQGAKETIKWTAPAAALYGRFT 324
YIHPDLRAANLLVGNELCKIAEFLALITFNTAQGAKETIKWTAPAAALYGRFT 324
QY .....

Db 121 YIHPDLRAANLLVGNELCKIAEFLALITFNTAQGAKETIKWTAPAAALYGRFT 324
YIHPDLRAANLLVGNELCKIAEFLALITFNTAQGAKETIKWTAPAAALYGRFT 324
QY .....

Db 450 KSDVMSFGILLQTELTVTKGRVPYPMVNNREVLQVGRGYMPCQCPSEDELMLCKK 500
KSDVMSFGILLQTELTVTKGRVPYPMVNNREVLQVGRGYMPCQCPSEDELMLCKK 500
QY .....

Db 181 KSDVMSFGILLQTELTVTKGRVPYPMVNNREVLQVGRGYMPCQCPSEDELMLCKK 500
KSDVMSFGILLQTELTVTKGRVPYPMVNNREVLQVGRGYMPCQCPSEDELMLCKK 500
QY .....

Db 510 DPDERPTEYIQSLE 525
DPDERPTEYIQSLE 525
QY .....

Db 241 DPDERPTEYIQSLE 256
DPDERPTEYIQSLE 256
QY .....

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[illegible][illegible]

Query Match

Best Local Similarity 97.94 Score 18.96 Gap 11 Length 544  
Matches 241 Conserved 194 Mismatches 5 Indels 0 Gaps 0

DB 256 IPRESLRDLVRLGQCGFGVWMTGNITKVAIKTLKPGIMPEAFLELAQIMKKLRHDK 325  
QY 1 IPRESLRDLVRLGQCGFGVWMTGNITKVAIKTLKPGIMPEAFLELAQIMKKLRHDK 325  
DB 426 LVPLVAVVSEPIYIVTEFWIKGSLDELKEGSGKFLKLPOLVDMAAQIADGMAYIERM 385  
QY 1 LVPLVAVVSEPIYIVTEFWIKGSLDELKEGSGKFLKLPOLVDMAAQIADGMAYIERM 385  
DB 446 YIHRDLRAANILVGNLVCKIADFGIARLIIPNEYTARTCAFETPKNALIAALAA 446  
QY 1 YIHRDLRAANILVGNLVCKIADFGIARLIIPNEYTARTCAFETPKNALIAALAA 446  
DB 448 KSDVWSFGILITELTKGRVPYGMVNVREVLEQVERGYRMVTPVTFESHELMK 448  
QY 1 KSDVWSFGILITELTKGRVPYGMVNVREVLEQVERGYRMVTPVTFESHELMK 448  
DB 509 DPDERPTFEYIQSFLE 523  
QY 1 DPDERPTFEYIQSFLE 523  
DB 241 DPDERPTFEYIQSFLE 256  
QY 1 DPDERPTFEYIQSFLE 256

RESULT 7

ID YES\_XIPHE STANDARD PRT: 544 AA.

AC P27447:

DT 01-AUG-1992 (REL. 23, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)

DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (P01-YES)

GN YES

CS ALPHAPHORUS HELLERI

SC LUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; MAMMALS

OC OSTREICHTHYES; ACTINOPTERYGII; ATHERINIFORMES

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-RIO LANCETILLA

RX MEDLINE: 91187436

RA HANNIG G., OTTILIE S., SCHARIL M.

RE ONCOGENE 6:361-369(1991).

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE KINASE

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN

CC -1- SIMILARITY: CONTAINS 1 SH4 DOMAIN

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC EMBL: X54970; G4484; -

DR HSP: P06241; LSHE

DR PROSITE: P00107; PROTEIN\_KINASE\_ATP; 1

DR PROSITE: P00109; PROTEIN\_KINASE\_TYR; 1

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1

DR PROSITE: PS50001; SH2; 1

DR PROSITE: PS50002; SH3; 1

KW PROTO-ONCOGENE; TYROSINE-PROTEIN KINASE; PHOSPHORYLATION

KW TRANSFERASE; ATP-BINDING; MYRISTYLATION; SH2 DOMAIN; SH3 DOMAIN

FT LIPID 2 153

FT DOMAIN 92 153

FT DOMAIN 159 256

FT NP\_BIND 278 531

FT BINDING 284 292

FT ACT\_SITE 306 306

FT MON\_PES 397 397

FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY)

SO SEQUENCE 544 AA; 61288 MW; 489624 CRC32

Query Match

Best Local Similarity 96.18 Score 18.67 Gap 11 Length 544

Matches 241 Conservative 11 Mismatches 4 Indels 0 Gaps 0

DB 273 IPRESLRDLVRLGQCGFGVWMTGNITKVAIKTLKPGIMPEAFLELAQIMKKLRHDK 325

QY 1 IPRESLRDLVRLGQCGFGVWMTGNITKVAIKTLKPGIMPEAFLELAQIMKKLRHDK 325

DB 333 LVPLVAVVSEPIYIVTEFWIKGSLDELKEGSGKFLKLPOLVDMAAQIADGMAYIERM 385

QY 1 LVPLVAVVSEPIYIVTEFWIKGSLDELKEGSGKFLKLPOLVDMAAQIADGMAYIERM 385





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DI 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SRC (PC 2.7.1.112) (16)
GN V-SRC:
GC AVIAN SARCOMA VIRUS (STRAIN 81),
OC VIRIDAE: SS-RNA ENVELOPED VIRUSES: POSITIVE-STRAND: RETROVIRIDAE.
OC ONCOVIRINAE.
KN [1]
RP SEQUENCE FROM N.A.
PX MEDLINE: 87064539.
RA IKAWA S., HAGINO-YAMAGISHI K., KAWAI S., YAMAMOTO T., TOSHIKAWA K.
RL MOL CELL BIOL 6:2420-2428(1986).
CC -1- FUNCTION: THIS PHOSPHOPROTEIN, REQUIRED FOR BOTH THE INITIATION
CC AND THE MAINTENANCE OF NEOPLASTIC TRANSFORMATION, IS A PROTEIN
CC KINASE THAT CATALYZES THE PHOSPHORYLATION OF TYROSINE RESIDUES
CC IN VIRO.
CC -1- CATALYTIC ACTIVITY: ATP -> A PROTEIN TYROSINE ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN, BELONGS TO THE SRC SUBFAMILY.
DR PIR: A25375; IYFVSL.
DR HSSP: P00524; 1PRL.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR TYROSINE-PROTEIN KINASE: TRANSFORMING PROTEIN INHERENT
DR TRANSFERASE; PHOSPHORYLATION: ATP-BINDING: KINETICALLY N.
KW SH3 DOMAIN; SH2 DOMAIN.
FT LIPID 2
FT DOMAIN 81 142
FT DOMAIN 148 245
FT DOMAIN 267 520
FT N-TERMO 273 281
FT BINDING 295 295
FT ACT_SITE 386 386
FT MOD_RES 416 416
SC SEQUENCE 568 AA; 63632 MW; 7FC6BD52 CMO42.

Query Match 92.7%; Score 1801; DB 1; Length 568
Best Local Similarity 89.1%; Pred. No. 0.00+00;
Matches 228; Conservative 17; Mismatches 11; Indels 18

DB 262 IPRESLRLEVKLGQCFCGEVWNGTWNGTIRVAIKTIKDTMSPEAFGLFAV...
QY 1 IPRESLRLEVKLGQCFCGEVWNGTWNGTIRVAIKTIKDTMSPEAFGLFAV...
DB 322 LVRLVAVYSEPIVIVITYMKSGLILFLKDMKRYLPLGLVIMRAALIAS...
QY 61 LVPLVAVYSEPIVIVITYMKSGLILFLKDMKRYLPLGLVIMRAALIAS...
DB 382 YVHRDLRAANILVGENLVCKVAIDPLAFETREYELAKQAKETWIAHAIY...
QY 121 YVHRDLRAANILVGENLVCKVAIDPLAFETREYELAKQAKETWIAHAIY...
DB 442 KSNVWSFGILLITELTKGRVPYPCYVKNREVLIVETRYDHP...
QY 181 KSNVWSFGILLITELTKGRVPYPCYVKNREVLIVETRYDHP...
DB 502 DPERPTEFYQSFLE 517
QY 241 DPERPTEFYQSFLE 256

RESULT 11
ID SRC-AVIS2
AC P15054;
DI 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

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\*\*\*\*\*  
Release 3.1A John F. Collins, BioComputing Research Unit  
University of Edinburgh, UK  
Distribution rights by Oxford Molecular Ltd  
\*\*\*\*\*  
Search\_PEP protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed Jan 13 1999, MapPar time 17.54 Secs ds  
726.596 Million cell updates/sec  
Tabular output not generated.  
Title: >US-08-955-841-4  
Description: (1-256) from US99.11941.pep  
Perfect Score: 1943  
Sequence: LIPRESLRLEVKLGQCGEV.....CWKKDPERIFEFYQSFLE 256  
Scoring table: PAM 120  
Gap 11  
Searched: 155420 seqs, 497956 residues  
Post-processing: Minimum Match 0%  
Listing first 45 sequences  
Database: sptrembl6  
1:sp\_mitochondria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_orqueall  
9:sp\_phase 10:sp\_pl 11:sp\_procent 12:sp\_punclassifi d  
13:sp\_virtobrate 14:sp\_virus  
Statistics: Mean 46.767; Variance 36.013; scale 0.467  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.  
SUMMAP is

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	1931	99.4	812	Q61466	COMPLETE GENOME.	0.0000
2	1802	92.7	533	Q98915	GENE C-SPC PROTEIN KINASE	0.0000
3	1793	92.4	533	Q98915	C-SPC	0.0000
4	1759	92.4	587	Q94917	LYSINE-TYROSINE KINASE	0.0000
5	1759	90.5	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
6	1752	90.2	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
7	1733	89.7	537	Q94917	LYSINE-TYROSINE KINASE	0.0000
8	1732	89.1	534	Q94917	LYSINE-TYROSINE KINASE	0.0000
9	1723	88.7	521	Q94917	LYSINE-TYROSINE KINASE	0.0000
10	1717	88.4	527	Q94917	LYSINE-TYROSINE KINASE	0.0000
11	1715	88.3	545	Q94917	LYSINE-TYROSINE KINASE	0.0000
12	1714	88.1	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
13	1714	87.9	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
14	1708	87.4	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
15	1595	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
16	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
17	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
18	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
19	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
20	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000

\*\*\*\*\*  
ALIGNMENTS  
RESULT 1  
ID Q85466 PRELIMINARY; PRT: 812 AA.  
AC Q85466;  
CT 01-NOV-1996 (TPREMBLREL. 01, CREATED)  
DI 01-NOV-1996 (TPREMBLREL. 01, LAST SEQUENCE UPDATE)  
DT 01-JUN-1998 (TPREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE COMPLETE GENOME.  
GS AVIAN SAPCOMA VIRUS.  
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND, RETROVIRAL  
QC UNCOVIRINAE.  
RN [1]  
RF MEDLINE: 82195528.  
RA KITAMURA N., KITAMURA A., TOYOSHIMA K., HIRAYAMA Y., YOSHIDA M.  
NAIPE 237.205-208(1982).  
EMBL: J02027; G209737; -  
DR PROSITE: PS00107; PROTEIN\_KINASE\_AIP; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PFAM: PF00017; SH2.  
DR PFAM: PF00018; SH3.  
DR PFAM: PF00069; pkinase.  
KW POLYPROTEIN.  
SQ SEQUENCE 812 AA; 88611 MW; 354955A CRC32;  
Query Match 99.4%; Score 1931; DB 14; Length 812  
Best Local Similarity 99.4%; Pred. No. 0.0000;  
Matches 155; Conservative 3; Mismatches 1; Indels 0

DB	Score	Query Match %	Length	ID	Description	Pred. No.
546	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
1	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
606	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
61	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
666	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
121	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
726	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
181	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000

\*\*\*\*\*  
BLK-PROTEIN TYROSINE K  
DSRC41.  
F49B2.5.  
SPC RELATED TYROSINE K  
INTEGRAL TYROSINE K  
H-PEP SRC-HOMOLOG TY  
TYR SH2  
SPC-RELATED INTEGRAL  
PROTO-ONCOGENE TYROSIN  
FACILITATE TYROSIN  
LIP29  
REC-FAMILY KINASE  
PROTEIN TYROSINE KINAS  
NON-RECEPTOR PROTEIN  
PROTEIN TYROSINE KINAS  
BTK/BMX CYTOSOLIC TYRO  
RECEPTOR TYROSINE KIN  
TYROSINE KINASE G47 R  
PROTEIN TYROSINE KINAS  
HVL TYROSINE KINASE  
PROTEIN TYROSINE KINAS  
RECEPTOR TYROSIN KINAS  
EPH-LIKE RECEPTOR TYRO  
VNR-NONRECEPTOR PROTEI

DB	Score	Query Match %	Length	ID	Description	Pred. No.
546	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
1	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
606	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
61	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
666	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
121	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
726	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000
181	1583	81.3	525	Q94917	LYSINE-TYROSINE KINASE	0.0000





[illegible]

[illegible]

322 LVQLYAVWSEEPYIVIEYMSKGSLLPHIKGFMCKVINDV

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RP SEQUENCE FROM N.A.
RX MEDLINE: 96182936.
RA TATOSYAN A., YATSULA B., SHUTMAN M., MOINOVA E., KAVERINA I.,
RA MUSATKINA E., LESKOV K., MIZENINA O., ZUEVA E., CALOITHY G.,
RA DEZELER P.
RL VIBROLOGY 216:347-356(1996).
DR EMBL: X84074; G663084.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_IYR; 1.
DR PFAM: PF00017; SH2.
DR PFAM: PF00018; SH3.
DR PFAM: PF00069; PKINASE.
DR PFAM: PF00069; PKINASE.
SQ SEQUENCE 545 AA; 61037 MW; D53537B6 CRC32;

Query Match      88.3%; Score 1710; DB 14; Length 545;
Best Local Similarity 84.7%; Pred. No. 3.95e-302;
Matches 216; Conservative

DB 282 IPRESLRLEVLKGGCGFGEVVMGWTNGTIRVAIKTLKPGTMSPEAFLOEQAVKVKLHEK
QY 1 IPRESLRLEVLKGGCGFGEVVMGWTNGTIRVAIKTLKPGTMSPEAFLOEQAVKVKLHEK
DB 342 LVOLYAVVSEEPYIVTEFTKSGLLDPLKEGEGFLKLPVLVDMAQIADQWAVIAD
QY 61 LVPLXAVVSEEPYIVTEFTKSGLLDPLKEGEGFLKLPVLVDMAQIADQWAVIAD
DB 402 YVHPDLRAANILVGENLECKVADFGIARLIEHEY-AR-3AFFFAKATIEEMHVA
QY 121 YVHPDLRAANILVGENLECKVADFGIARLIEHEY-AR-3AFFFAKATIEEMHVA
DB 462 KSDVMSFGILLIETIKGRVFPYPMGNSEVLDPVEGVPMPGPPGEPESLHLMK
QY 181 KSDVMSFGILLIETIKGRVFPYPMGNSEVLDPVEGVPMPGPPGEPESLHLMK
DB 522 EPEPTPEFYLOAQI 536
QY 241 DPDERPTFEYIQSFL 255

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RESULT 12 PRELIMINARY; PRI: 545 AA.
ID Q86363.
AC Q86363.
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DI 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
ET 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE 256 LKSDVMSFGILLIETIKGRVFPYPMGNSEVLDPVEGVPMPGPPGEPESLHLMK
QY 1 IPRESLRLEVLKGGCGFGEVVMGWTNGTIRVAIKTLKPGTMSPEAFLOEQAVKVKLHEK
DB 316 LVOLYAVVSEEPYIVTEFTKSGLLDPLKEGEGFLKLPVLVDMAQIADQWAVIAD
QY 61 LVPLXAVVSEEPYIVTEFTKSGLLDPLKEGEGFLKLPVLVDMAQIADQWAVIAD
DB 376 YVHPDLRAANILVGENLECKVADFGIARLIEHEY-AR-3AFFFAKATIEEMHVA
QY 121 YVHPDLRAANILVGENLECKVADFGIARLIEHEY-AR-3AFFFAKATIEEMHVA
DB 462 KSDVMSFGILLIETIKGRVFPYPMGNSEVLDPVEGVPMPGPPGEPESLHLMK
QY 181 KSDVMSFGILLIETIKGRVFPYPMGNSEVLDPVEGVPMPGPPGEPESLHLMK
DB 522 EPEPTPEFYLOAQI 536
QY 241 DPDERPTFEYIQSFL 255

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US-08-955-841-4.rspt

Query Match  
Best Local Similarity 86.3%; Score 1708; DR 14; Length 524;  
Matches 220; Conservative 20; Mismatches 12; Indels 4; Gaps 0

DB 262 IPRESRLKLVKGGCGCEVVMGTWNGTTTVAIKTLKPTMTSPKAPLOEALVKKLHKK 421  
QY 1 IPRESRLKLVKGGCGCEVVMGTWNGTTTVAIKTLKPTMTSPKAPLOEALVKKLHKK 421  
DB 322 LVOLYAVVSEPTIYIVIEYMSKGLDLFLK---GKYLRLPOLVMAAOIASMAVYHNN 428  
QY 61 LVPLYAVVSEPTIYIVIEYMSKGLDLFLK---GKYLRLPOLVMAAOIASMAVYHNN 428  
DB 379 YVHRLRAANILVGENLVCKVADPGLAPITPTTAKGAKPKIWTAPFAALYGRFTI 438  
QY 121 YVHRLRAANILVGENLVCKVADPGLAPITPTTAKGAKPKIWTAPFAALYGRFTI 438  
DB 439 KSDVNSFGILLITLTITKGRMPYPMGNGEVLDRVERGYRMPGPPPESTHMAVYHNN 449  
QY 181 KSDVNSFGILLITLTITKGRMPYPMGNGEVLDRVERGYRMPGPPPESTHMAVYHNN 449  
DB 499 DPEERPTFEYLQAOL 513  
QY 241 DPEERPTFEYLQAOL 513

RESULT 15  
ID 039851 PRELIMINARY; PRT: 563 AA.  
AC 039851;  
DI 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DI 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DI 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE GARDNER-RASHEED FELINE SARCOMA VIRUS  
DE (GR-FESV) V-FGR ONCOGENE CODING FOR P70-GAT-FGR TRANSPORIN-FAV  
DE PROTEIN (GR-FESV)  
OS FELINE SARCOMA VIRUS (GARDNER-ARNSSTEIN FELINE INFECTIA ON V-FAV)  
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE  
CC UNOVIKINAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 84097512.  
RA NAHARPO G., ROBRINS K.C., RENDY P.E.;  
RI SCIENCE 223:63-66(1984);  
DR EMBL; K01487; G323895;  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS01132; ACTINS\_ACT-LIKE; 1.  
DR PFAM; PF00017; SH2.  
DR PFAM; PF00022; Actin.  
DR PFAM; PF00069; PKinase.  
KW POLYPROTEIN; STRUCTURAL PROTEIN.  
SQ SEQUENCE 663 AA; 74916 MW; F6B1A64D CRC32;

Query Match  
Best Local Similarity 82.0%; Score 1593; DR 14; Length 524;  
Matches 203; Conservative 26; Mismatches 27; Indels 1

DB 399 ISRSSTLQRLGTCFGDVMGLGMWNSIKVAVKTIKPTMTSPKAPLOEALVKKLHKK 421

US-08-955-841-4.rspt

Query Match  
Best Local Similarity 86.3%; Score 1708; DR 14; Length 524;  
Matches 220; Conservative 20; Mismatches 12; Indels 4; Gaps 0

DB 262 IPRESRLKLVKGGCGCEVVMGTWNGTTTVAIKTLKPTMTSPKAPLOEALVKKLHKK 421  
QY 1 IPRESRLKLVKGGCGCEVVMGTWNGTTTVAIKTLKPTMTSPKAPLOEALVKKLHKK 421  
DB 322 LVOLYAVVSEPTIYIVIEYMSKGLDLFLK---GKYLRLPOLVMAAOIASMAVYHNN 428  
QY 61 LVPLYAVVSEPTIYIVIEYMSKGLDLFLK---GKYLRLPOLVMAAOIASMAVYHNN 428  
DB 379 YVHRLRAANILVGENLVCKVADPGLAPITPTTAKGAKPKIWTAPFAALYGRFTI 438  
QY 121 YVHRLRAANILVGENLVCKVADPGLAPITPTTAKGAKPKIWTAPFAALYGRFTI 438  
DB 439 KSDVNSFGILLITLTITKGRMPYPMGNGEVLDRVERGYRMPGPPPESTHMAVYHNN 449  
QY 181 KSDVNSFGILLITLTITKGRMPYPMGNGEVLDRVERGYRMPGPPPESTHMAVYHNN 449  
DB 499 DPEERPTFEYLQAOL 513  
QY 241 DPEERPTFEYLQAOL 513

RESULT 15  
ID 039851 PRELIMINARY; PRT: 563 AA.  
AC 039851;  
DI 01-JAN-1998 (TREMBLREL. 05, CREATED)  
DI 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  
DI 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)  
DE GARDNER-RASHEED FELINE SARCOMA VIRUS  
DE (GR-FESV) V-FGR ONCOGENE CODING FOR P70-GAT-FGR TRANSPORIN-FAV  
DE PROTEIN (GR-FESV)  
OS FELINE SARCOMA VIRUS (GARDNER-ARNSSTEIN FELINE INFECTIA ON V-FAV)  
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE  
CC UNOVIKINAE.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 84097512.  
RA NAHARPO G., ROBRINS K.C., RENDY P.E.;  
RI SCIENCE 223:63-66(1984);  
DR EMBL; K01487; G323895;  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS01132; ACTINS\_ACT-LIKE; 1.  
DR PFAM; PF00017; SH2.  
DR PFAM; PF00022; Actin.  
DR PFAM; PF00069; PKinase.  
KW POLYPROTEIN; STRUCTURAL PROTEIN.  
SQ SEQUENCE 663 AA; 74916 MW; F6B1A64D CRC32;

Query Match  
Best Local Similarity 82.0%; Score 1593; DR 14; Length 524;  
Matches 203; Conservative 26; Mismatches 27; Indels 1

DB 399 ISRSSTLQRLGTCFGDVMGLGMWNSIKVAVKTIKPTMTSPKAPLOEALVKKLHKK 421

Top







[illegible]



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719 TATTTGAGAGAGGTTTGGAAAGAGCTGCTGGCAGGGCAATGATATTGTTG 768
812 TGAATGTTCTCTAAAGTCCAGACTGGAGTACAGAGGAAGAGCAGGACTTC 861
769 TGAAGATGTTCTAAAGTTGTTGCTGGAGTACAGAGGAAGAGCAGGACTTC 818
862 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 911
819 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 869
912 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
919 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 869
869 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
962 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
919 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 869
1012 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1019 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1062 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1069 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1112 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1119 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1162 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1169 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1212 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1219 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1262 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1269 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1312 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1319 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1362 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1369 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1412 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1419 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1462 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1469 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1512 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1519 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1562 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1569 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1612 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861
1619 AATGAAGATGTTCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 861

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1708 ACATGSGIGICCCCAACAATGGAGGGAATGAGGCGGCGGCGGICGACAAATAA 1757
1669 ACAATGATGCTCCCAACAATGGAGGGAATGAGGCGGCGGCGGICGACAAATAA 1718
1758 GTTTATTATGAAAAAATAAATAAATAAATAAATAA 1789
1719 GTTTATTATGAAAAAATAAATAAATAAATAAATAA 1750
chen.gcg          check: 2569 from: 82    to: 1789  /Reverse
GB_P2:HS025816   check: 2569 from: 1     to: 2505
G19940 human SIS A002640, sequence tagged site, 7/96
Gaps: 1 Quality: 1895 Pct: 9.219 Score: 160 Width: 3 Limit: 1/2
1693 GTTTCAGGCTGCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 1644
14 CTGAGGCTGCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 63
1643 GAGGCTGCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 1595
64 GAGGCTGCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 113
1644 GAGGCTGCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 163
1544 TGTGAGGCTGCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 1495
164 TGTGAGGCTGCTGAGGCTGCTGAGGATTTCTGGATCCCAATGTGCTCC 213
1494 AAGGATAGG 1486
214 AAGGATAGG 222
chen.gcg          check: 2569 from: 1     to: 1789  /Reverse
GB_P2:HS025816   check: 2569 from: 2369 to: 2505
G25816 Human TATA-binding protein associated factor 11 30 (TAF11L) gene, complete
Gaps: 1 Quality: 1895 Pct: 9.219 Score: 160 Width: 3 Limit: 1/2
1773 TTTTTCATATAAATAAATAAATAAATAAATAAATAA 1724
2402 TGTTCATATAAATAAATAAATAAATAAATAAATAA 2453
1723 TTGGGAGACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 1674
2452 TTGGGAGACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 2501
1673 GGCACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 1637
2502 GGCACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 2539
chen.gcg          check: 2569 from: 1     to: 1789  /Reverse
GB_P2:HS025816   check: 2569 from: 2369 to: 2505
G25816 Human TATA-binding protein associated factor 11 30 (TAF11L) gene, complete
Gaps: 1 Quality: 1895 Pct: 9.219 Score: 160 Width: 3 Limit: 1/2
1773 TTTTTCATATAAATAAATAAATAAATAAATAAATAA 1724
2402 TGTTCATATAAATAAATAAATAAATAAATAAATAA 2453
1723 TTGGGAGACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 1674
2452 TTGGGAGACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 2501
1673 GGCACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 1637
2502 GGCACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 2539
1673 GGCACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 1637
2502 GGCACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 2539
1626 AGTACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 1577
2552 AGTACACATGTTGTAATGATCAAAAGCTCTGAGGCGGCGGCGGICG 2501
1576 GAGG 1573

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chen.acg          check: 2569 from: 1 to: 1789
SB_P2:AF007793    check: 525 from: 2569 to: 4367
AF007793 Zoa mays retinoblastoma-related protein 1 (RPR1) mRNA, complete cds. 9/
Gaps: 0 Quality: 278 Ratio: 8.968 Score: 26 Width: 18 Limits: +/-19

1759 TTTATTATGAAAAAATAAAAAAAAAAAAAA 1789
|||||
4328 TTGATGTAAGAAAAAATAAAAAAAAAAAAAA 4358

chen.acg          check: 2559 from: 1 to: 1789 /Reverse
SB_P2:G37984      check: 3521 from: 52 to: 307
G37984 c3m58 plasmodium falciparum haploid Plasmodium falciparum STS genomic, se
Gaps: 0 Quality: 260 Ratio: 10.009 Score: 26 Width: 10 Limits: +/-11

1789 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 1764
|||||
53 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 78

chen.acg          check: 2569 from: 1 to: 1789 /Reverse
SB_P2:HMU91221    check: 8436 from: 2552 to: 250633
HMU91221 Human Chromosome 16 BAC clone C11987SK-A-363E6, complete sequence. 3/98
Gaps: 2 Quality: 269 Ratio: 9.974 Score: 26 Width: 11 Limits: +/-12

1789 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 1740
|||||
2552 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 25589

1739 GGTGATGCGGTCGCA ..GTTTGGAGACACATGATGTCGCAAGTGA 1699
|||||
24590 GGCATATTTGCTTAAG..TGGTGTCAAACTCTCTGAGGCTCAAGTGA 25633

chen.acg          check: 2560 from: 1 to: 1789 /Reverse
SB_P2:HUAC09093    check: 8071 from: 127925 to: 130381
AC09093 Human Chromosome 16 BAC clone C11987SK-254P9, complete sequence. 3/98
Gaps: 2 Quality: 277 Ratio: 9.278 Score: 26 Width: 10 Limits: +/-11

1789 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 1740
|||||
127925 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 127963

1739 GGTGATGCGGTCGCA ..GTTTGGAGACACATGATGTCGCAAGTGA 1699
|||||
127964 GGCATATTTGCTTAAG..TGGTGTCAAACTCTCTGAGGCTCAAGTGA 128007

chen.acg          check: 2569 from: 326 to: 1789
SB_P2:HSU97680     check: 6241 from: 1 to: 1462
HSU97680 Homo sapiens cyclin A1 mRNA, partial cds. 6/97
Gaps: 1 Quality: 260 Ratio: 9.179 Score: 26 Width: 8 Limits: +/-9

1750 ACAATAAA.....GTTTATTATGAAAAAATAAAAAAAAAAAAAA 1788
|||||
1420 ACAATAAACTGTTTGTCTTAAGAAAAAATAAAAAAAAAAAAAA 1462

chen.acg          check: 2569 from: 1 to: 1789 /Reverse
SB_P2:HS511E16     check: 8865 from: 24543 to: 56632
AL023694 Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contain
Gaps: 2 Quality: 263 Ratio: 9.183 Score: 26 Width: 21 Limits: +/-22

1789 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 1740
|||||
24544 TTTTTHHHHHHHHHHHHHHHHHHHHHHHHH 24581

1739 GGTGATGCGGTCGCA ..GAGACACCAATGTCGCAAGTGA 1699
|||||
24582 CAGTGGTTCGCTATGTTGAGTAACTTAACTCTCTGCTCAATGA 24625

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812 TGAAGGTGCTGAAGTTCTGAGACGGAGTACAAAGGAGAGACGAGGACTTC 861
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
813 TGAAGGTGCTGAAGTTCTGAGACGGAGTACAAAGGAGAGACGAGGACTTC 818
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
862 AATGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 911
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
814 AATGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 868
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
912 AGTGTAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 961
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
864 AGTGTAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 918
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
962 CACACTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTG 1011
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
914 CACACTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTG 968
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1012 AATGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 1061
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
964 AATGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 1018
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1016 AATGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 1065
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1018 AATGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 1068
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1112 CACACTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTG 1161
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1064 CACACTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTG 1118
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1116 AGCAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1211
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1118 AGCAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1168
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1212 ACCGTGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1261
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1164 ACCGTGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1218
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1216 ACAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1311
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1218 ACAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1268
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1312 GTGAAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1361
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1264 GTGAAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1318
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1316 CAAGTGTGATGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1411
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1318 CAAGTGTGATGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1368
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1412 CTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1461
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1364 CTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1418
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1416 CTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1461
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1418 CTGATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAG 1468
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1512 GTAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1561
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1464 GTAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1518
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1516 GTAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1561
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1518 GTAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1568
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1612 TCAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1661
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1564 TCAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1618
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1616 TCAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1661
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1618 TCAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1668
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1710 ATGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1759
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1668 ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
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1760 TTATTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1789
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1718 GTTATTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1748
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

chen.gcg          check: 2569 from: 1 to: 1789 /Reverse
GB_P02489.479    check: 7000 from: 1 to: 220
GB_P02489.479    check: 7000 from: 1 to: 220
Gaps: 1 quality: 1935 ratio: 8.422 score: 150 width: 2 limit: 1000

1638 CTGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1644
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
14 CTGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1643 GAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1595
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1645 GAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1545
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114 GAAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1544 TCTGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1485
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
164 TCTGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 213
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1494 AAGGATAGG 1486
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
214 AAGGATAGG 222

chen.gcg          check: 2569 from: 29 to: 1789
GB_P02489.479    check: 1077 from: 1 to: 1750
GB_P02489.479    check: 1077 from: 1 to: 1750
Gaps: 1 quality: 1935 ratio: 8.422 score: 150 width: 2 limit: 1000

1672 CCAAGAGAGAGGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1720
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1632 CCAAGAGAGAGGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1681
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1721 CAACATGAGAGAGGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1770
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1682 CAACATGAGAGAGGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1731
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1771 AAAAAAAAAAAAAAAAAAAAAA 1789
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1732 AAAAAAAAAAAAAAAAAAAAAA 1750

chen.gcg          check: 2569 from: 1 to: 1789 /Reverse
GB_P02489.479    check: 4430 from: 2485 to: 2605
GB_P02489.479    check: 4430 from: 2485 to: 2605
Gaps: 1 quality: 1935 ratio: 9.511 score: 150 width: 2 limit: 1000

1773 TTTTTCATATAAACTTTATTGAGAGAGGAGGAGTCTGAGAGTCTGAGAGT 1724
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1402 TTTTTCATATAAACTTTATTGAGAGAGGAGGAGTCTGAGAGTCTGAGAGT 2451
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1723 TTTGAGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1674
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1452 TTTGAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 2501
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1673 CCAAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 1637
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1502 CCAAGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGT 2599
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

chen.gcg          check: 2569 from: 1 to: 1789 /Reverse
GB_P02489.479    check: 4430 from: 2485 to: 2605
GB_P02489.479    check: 4430 from: 2485 to: 2605
Gaps: 1 quality: 1935 ratio: 9.511 score: 150 width: 2 limit: 1000

1773 TTTTTCATATAAACTTTATTGAGAGAGGAGGAGTCTGAGAGTCTGAGAGT 1724

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[illegible]

Distribution

[illegible]

Wed Jan 19 12:06:57 1988

MesFartTime: 0.30 seconds  
448.805 Million Cell Spikes/sec

705-08-055-941-3

[illegible][illegible]

Scoring table: PAM 150  
Gap 11

Searched: 131922 seqs, 15150660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

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a-adenesq32
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[illegible]

## SUMMARIES

[illegible]

```

Db 409 sfavllweifsyrpypkmslksveasevkekympepdeqcpqpyhly mssawewcpqrll 408
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 SFGILLWEIYSFGFVYPRIPKDDVVPRVEKGYKMLAFERCTFPAVYEVNKN WLLGAAE 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 469 ppirklaeklar 480
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QY 241 PRFIQLPEOLEH 252
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RESULTS	3
ID	R71133 standard: Protein: 507 AA.
AA	R71133;
DT	27-OCT-1995 (first entry)
DE	Cytoplasmic tyrosine kinase.
KW	cytoplasmic; tyrosine kinase.
KW	screening; anticancer agent; SH3; Src homology domain.
KW	Hom sapiens.

Key Location/Qualifiers  
domain 48..111 /note= "SH3 domain"  
domain 122..196 /note= "SH2 domain"  
domain 233..478 /note= "tyrosine kinase domain"

W05506113-A.  
02-MAR-1995.  
25-AUG-1994; J01411.  
25-AUG-1993; JP-310403.  
29-MAR-1994; JP-058553.  
(ASAH ) ASahi Kasei Kogyo KK.  
Sakano S;  
WPI: 95-106842/14.  
N-PSDR: 084888.

Cytoplasmic tyrosine kinase and antibody recognising it as a  
screening chemical substances for tyrosine kinase inhibitory  
activating activity for use as cancer therapy

Claim 1: Page 42-44; 3pp; English.

A cytoplasmic tyrosine kinase which has enhanced expression in  
connection with blood cell differentiation has been isolated from  
human UT-7 blood cell line. The DNA sequence and amino acid  
sequence of the enzyme, are useful for screening agents for having  
inhibiting or activating activity on the tyrosine kinase. \*Of uses are  
Sequence 507 AA.

[illegible]

61 LLGVIVEKGGLYITEYMAKSLVDYLRSGRSLVQDGLPESLRYVTAMHLEENNF 129  
349 vhrdlaarnilvsdlvakvdsfqlakarkelddar|pywkyarcsa|klsrslg

121 VHRDLAARNVLSEEDNVAKVSDFGLTKKASSTQNTGKLPVNTATATALKKSTSLSNVW 160  
469 sfgrllwvfydrayppkmsikeysaeakyytqfpcapnybvlmssewcaqftr 468  
161 SFGILLWEISFGRPYPPIPLKDVVPVREYGYKMDAIDGCPVAVYEVAKNWHIAAMP 241  
469 ppfiklaeklar 480  
241 PFTIQLPEMIEH 252

JUL 4  
R71131 standard; Protein: 246 AA

RESULT	4
ID	R71131 standard; Protein; 246 AA.
AC	R71131.

1 20000195 (first entry)  
 2 TYROSINE KINASE domain of tyrosine tyrosine kinases  
 3 20000196 (first entry)  
 4 20000197 (first entry)  
 5 20000198 (first entry)  
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 7 20000200 (first entry)  
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 95 20000288 (first entry)  
 96 20000289 (first entry)  
 97 20000290 (first entry)  
 98 20000291 (first entry)  
 99 20000292 (first entry)  
 100 20000293 (first entry)

kinase encoding family of genes. Arg is expressed as xco transcodable by analogy with c-361, the alternative 1st and sequences have been designated A and B (Q14937) and it is assumed that they are joined to the arg second exon

The amino acid sequence is represented as found in the specification.  
Sequence 1-146 AA:

Query Match 47.0% Score 892; DB 3; Length 1146;  
Best Local Similarity 47.7%; Pred.No. 6,82e-77;  
Matches 123; Conservative 61; Mismatches 66; Indels 8; Gaps  
DDEDD 246 gddimzhkgggggygevyvyyakkslltysavtlldltltydceffkssatfeykqfsl  
QQY 1 NKKELKLIIQTIGKFEFGVMLGDVPG-N-KVAVKCIKNDATA-QAFLAFASVMTCLEHNS E  
DBB 308 llygllygtcllo-pfyivltortpygcilidyrcnrcrouttavilymatdlissarelek  
QQY 59 LVQLLGIVAEKGLLYIETYNAGKSLEYLESSEGSVLGGDCITKPSDYCEAMEYLSD  
DBB 317 kufhdraardcagchrvkvkdagistmmtsdutabafaykfkratesapartls  
QQY 319 KNFVFEDLAAPNVLSDENAKVDFFGTIK-EASS-TODSG-KLPNVTATPEALREYKE L  
DBB 427 sbsdrwafrgallwlatyymstrfeelltsyvullkyetmmegeregrffmvvelmd  
QQY 174 SKSLVWSPDLLWEINSPDPVPRFELLKVWSGVTVFWCDACDGGIFAMENMNNA  
DBB 487 kwspadrpsfaethafe 504  
QQY 224 HIDAAMPSSFIQLPEOLE 251

RESULT 6  
ID P94538 standard; Protein: 441 AA.  
AC R94538:  
DT 10-JUL-1996 (first entry)  
DE Drosophila Src28C tyrosine kinase.  
VE Cytosolic tyrosine kinase; BMX; haematopoietic cell  
KW cell growth; cell proliferation; tumour; diagnosis; therapy;  
KW Src28C.  
OS Drosophila melanogaster.  
ES Key Location/Qualifiers  
FT domain 1..55  
FT /label= SH3\_domain  
FT domain 55...155  
FT /label= SH2\_domain  
FT domain 186...425  
FT /label= Tyrosine\_kinase\_domain  
FT binding\_site 187..209  
FT /label= ATP-binding\_region  
FT modified\_site 332  
FT /label= Autophosphorylation\_site  
PI WC9611275-A1.  
PD 18-APR-1996.  
PF 09-OCT-1995; F10555.  
PF 07-OCT-1994; WS-320432  
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.  
AI Aitalo K;  
DI WPI; 96-209856/21.  
PT Cytoplasmic tyrosine kinase BMX and related DNA - useful to  
PT stimulate haematopoietic cell growth.  
PS Disclosure, Page 28-29; 40pp; English.  
CC The amino acid sequence (P94538) of Drosophila Src28C tyrosine  
CC kinase was compared with the sequences of 3 members of a  
CC newly-identified non-receptor tyrosine kinase family htk (P94544),  
CC trk (P94535) and TEC (P94536), and with novel human cytoplasmic  
CC tyrosine kinase BMX (see also P94533). Close homology was found.  
SQ Sequence 441 AA;

Query Match	45.6%	Score 865	DB "7"	Length 471
Best Local Similarity	43.5%	Pred. NO.	3,866	74
Matches 114	Conservative	66	Mismatches	73
			Index	9
			Cars	1

[illegible]

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FI	407..644	/label= Tyrosine-kinase_domain
FI	408..430	/label= ATP-binding_region
FI	551	/label= Autophosphorylation_site
FN	W09611275-A1.	
PD	18-APR-1996.	
PF	09-OCT-1995; FI0555.	
PR	07-OCT-1994; US-320432.	
PA	(UYHE-) UNIV HELSINKI LICENSING LTD OF.	
PI	Alitalo K;	
DR	WPI: 96-269856/21.	
PT	Cytoplasmic tyrosine kinase BMX and related DNA - useful to	
PT	stimulate hematopoietic cell growth.	
PS	Disclosure: Page 21-23, 40pp; English.	
CC	Cytoplasmic tyrosine kinase BTK (B94534) is selectively expressed	
CC	at certain stages of B-cell development.	
CC	and 2 other members of a newly-identified non receptor tyrosine	
CC	kinase family, ITK (B94535) and TEC (B94536), and of the	
CC	Drosophila Src28C tyrosine kinase (B94538), were compared with	
CC	that of novel cytoplasmic tyrosine kinase BMX (see also B94534).	
CC	Close homology was found.	
SC	Sequence 659 AA;	

[illegible]

RESULT	9
ID	W06708
AC	W06708; standard; Protein; 659 AA.
DT	04-FEB-1997 (first entry)





11 411-412: 424/211  
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CC (T00617), and used in the treatment and diagnosis of leukemia and thrombocytopenia.  
 CC sequence 675 AA;  
 Query Match 40.6%; Score 770; Len 15; Length 475;  
 Rest Local Similarity 43.5%; Pred. No. 177e-64;  
 Matches 113; Conservative 58; Mismatches 81; Indels 8;  
 Gaps 6;  
 Db 416 eilklkelsgdlqgvgqlgkqkqgdydkmkkeusmdcltqppgmkksqk  
 QY 4 ELKLITICGCEGDVNLGDYGN-KVAVKCKNIAIAUA-ELAFASVMDLPHKKA  
 Db 476 yavcskepp-yiviteyinsgcllylrshkqg-lepslllemydyvdmak  
 QY 62 LGVIVEKGLIVITEYMAKGSVDYLSKRSVIGDMLIKESTV-VIAMS  
 Db 534 hrdlaarncldrdlcvkvsdfamtryvlddyvssvsktpvssapv  
 QY 122 HRLAARNVLSVEDNNAKVSDFGLIKHASTQ--EI-G-KIPVWIAHFAHFA  
 Db 594 drwafgilmwefslqkqpydyldyuspykysqhllyrphlasp-lypms  
 QY 178 DWMSGILLWFYSGRPVPPPIKLVVFAVEKTYRMALG-VIAYVWVW  
 Db 654 ekrtfqqlssieplrek 674  
 QY 238 AMRPSFLOLEHINKE 257

RESULT 13  
 ID R94533 standard; Protein; 675 AA.  
 AC R94533;  
 DT 10-JUL-1996 (first entry)  
 DE BMX tyrosine kinase.  
 KW Cytoplasmic tyrosine kinase; BMX; haematopoietic cell  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT domain 1..212  
 FT /label= "N-terminal\_region"  
 FT /note= "The N-terminal region contains the  
 FT pleckstrin homology region consisting  
 FT of a 7-strand antiparallel beta-sheet."  
 FT domain 213..265  
 FT /label= SH3\_domain  
 FT domain 296..392  
 FT /label= SH2\_domain  
 FT domain 422..659  
 FT /label= Tyrosine\_kinase\_domain  
 FT binding\_site 423..445  
 FT /label= ATP-binding\_region  
 FT modified\_site 566  
 FT /label= Autophosphorylation\_site  
 FT /note= "corresponds to the Tyr411  
 FT autophosphorylation site of c-Src"  
 PN W09611275-A1.  
 PD 18-APR-1996  
 PF 09-OCT-1995; F10555.  
 PF 07-OCT-1994; US-320432.  
 PA (UYHE-) UNIV HELSINKI LICENSING LTD OF.  
 PI Alitalo K;  
 DR WPI: 96-209856/21.  
 PI Cytoplasmic tyrosine kinase BMX and related RNA - useful to  
 PI stimulate haematopoietic cell growth.  
 PS Claim 1: page 19-21; 40pp; English.  
 CC Novel cytoplasmic tyrosine kinase BMX (R94533) is capable of  
 CC stimulating growth and/or proliferation of hematopoietic cells.  
 CC It is the product of a cDNA clone isolated from a human bone marrow  
 CC cDNA library. It shares characteristics with members of the  
 CC FIP-1/BCR (see R4534-36) subfamily and with cranspallin (see  
 CC tyrosine kinase (R4538)). It is useful as a marker for cell  
 CC growth and differentiation, and for various types of tumor  
 CC formation, and in the diagnosis and treatment of diseases

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JH0559 #type complete  
protein-tyrosine kinase (EC 2.7.1.112) OSK - human  
Protein-tyrosine kinase 67L Protein-tyrosine kinase 67L  
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30-Jun-1992 #sequence\_18-Sep-1998 #date\_created  
18-Sep-1998  
JH0559; S38818, S39044; S19025  
JH0559  
Braeuninger, A.; Holtrich, U.; Streibhardt, K.;  
Ruebsamen-Waigmann, H.  
Gene (1992) 110:205-211.  
Isolation and characterization of a human gene that encodes  
new subclass of protein tyrosine kinases.  
ces MUID:92165060

## SUMMARIES

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REFERENCE
#journal Brauningner, A.; Karn, T.; Strebhardt, K.;
#authors Fuehsamer-Walgmann, H.
#title Oncogene (1993) 8:1365-1369
#journal Characterization of the human Cxk locus.
#accession S38818
#status preliminary
#molecule_type DNA
#residues 1-450 #label BF2
#cross-references EMBL:X74765
REFERENCE
#journal Parkanen, J.; Armstrong, E.; Berglund, M.;
#authors Hirvonen, H.; Haenker, K.; Anttilä, K.
#journal Oncogene (1994) 9:2013-2018
#title cys encodes a putative cytoplasmic tyrosine
#comment The conserved tyrosine at the phosphorylation
#site (src).
#cross-references NIDB:9-050797
#accession SI9024
#status preliminary
#molecule_type mRNA
#residues 1-450 #label PAR
#cross-references EMBL:X7474; NIDB:9004; NIDB:9015
REFERENCE
#journal Holtsch, T.; Brackmann, A.; Ziehlmann, P.;
#authors Ruebsamen-Walgmann, H.
#journal Proc. Natl. Acad. Sci. USA (1994) 91:104
#title
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**Title
Exp additional protein-tyrosine kinases expressed in human
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June 1997
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CDR-CKK
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MIM:11642; MIM:12495
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ATP: phosphorylation: tyrosine-specific protein kinase
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21-171
domain SH2 homology #label SH2
184-447
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201-223
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GV 1 NMFKELITGKGFSDVGLGKRGKVAVKTNINIAAQAFLAASVWLEHNNI
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Mus musculus #common_name mouse
DATE
15-Jun-1996 #sequence_revision 30-Jun-1996 #text_update
09-Apr-1998
ACCESSIONS
I48929; S50498
REFERENCE
#authors
Kjaer, S., Adam, D., Glass, K., Farquhar, J., Bolen, J.,
Penhallow, R.C.
#journal
Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2697-2699
#title
Csk: a protein-tyrosine kinase related to csk that defines an
enzyme family

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**cross-references
MIM:91226538
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PT0183
#authors
Lai, C., Lemke, G.
#journal
Neuron (1991) 6:691-704
#title
An extended family of protein-tyrosine kinase genes
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**accession
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homology: SH2 homology: SH3 homology:
ATP: autophosphorylation: phosphorylation: phosphotyrosine
tyrosine-specific protein kinase
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16-65
domain SH3 homology #label SH3
21-171
domain SH2 homology #label SH2
184-447
domain protein kinase homology #label KIN
201-223
region protein kinase ATP-binding motif
222
active site Lys #status predicted
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Best Local Similarity 98.48 Pred. No. 0.00e+00
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GV 1 NMFKELITGKGFSDVGLGKRGKVAVKTNINIAAQAFLAASVWLEHNNI
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GV 61 LLGVIVFEGKGLYIVTEYMAKSLVLYLSKRSVLPFUTLKEISLVYEMAYLENNI
DB 311 VHRDLAARNVYSEFNVAKVSDFGTLKASSTGGLKLVAVIAEALRKKESVW
GV 121 VHRDLAARNVYSEFNVAKVSDFGTLKASSTGGLKLVAVIAEALRKKESVW
DB 371 STGILLWEIYSPGVYPRIPKLVVVERKSKMLADGCPVAVIYKNNWHILAAAR
GV 181 STGILLWEIYSPGVYPRIPKLVVVERKSKMLADGCPVAVIYKNNWHILAAAR
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GV 241 PTELOLRQLEHITHREL 258

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[illegible]





[illegible]

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10







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DB 229 DLGHLILGAGIGEGEFCAGVLOGEYLVQKAVYKINQNTACAFDETAFTAVKLEHNLVA 188
QY 1 NMKELKLLQIGKGEFGDVMGDPGNKVAVKCIKNDATAQAFLAASVNTQLRHSNLVQ 60
DB 299 LQGVILHH--GLYIVVHEVSKGNLVNLFRTGPAIVSTLLQALHVAEGMEVLESVK 377
QY 61 LLGVVVEEKGGIVIVTEYMAKGSIVDYLSPGSPSVLGGSCILKFSLDVCEAMVLEGNF 120
DB 347 VHRDLAARNLVSEDLVAKVSDPGLAKAEFLKGLDSSPIPVKWTAEALFNSEFSEKSV 367
QY 121 VHRDLAARNLVSEDLVAKVSDPGLK--FASSTLVLSKLVKWTADPAPEYFETKSV 109
DB 368 WSGVILWEVSGVGRAPYKMSLKEVSEAVEKGVKPEPDPSPGVVHIMSCWEAEPSR 427
QY 180 WSPGILLWEVSGVGRAPYKMSLKEVSEAVEKGVKPEPDPSPGVVHIMSCWEAEPSR 427
DB 428 RPPFRKIVEKLR 440
QY 240 RPSFLQIREQLEH 252

Query Match 59.6%, Score 1132, DB 1: Length 407;
Rest local similarity 57.3%; Pred No. 1,998,241;
Matches 145; Conservative 55; Mismatches 50; Indels 3; Gaps 2;

DB 229 DLGHLILGAGIGEGEFCAGVLOGEYLVQKAVYKINQNTACAFDETAFTAVKLEHNLVA 188
QY 1 NMKELKLLQIGKGEFGDVMGDPGNKVAVKCIKNDATAQAFLAASVNTQLRHSNLVQ 60
DB 299 LQGVILHH--GLYIVVHEVSKGNLVNLFRTGPAIVSTLLQALHVAEGMEVLESVK 377
QY 61 LLGVVVEEKGGIVIVTEYMAKGSIVDYLSPGSPSVLGGSCILKFSLDVCEAMVLEGNF 120
DB 347 VHRDLAARNLVSEDLVAKVSDPGLAKAEFLKGLDSSPIPVKWTAEALFNSEFSEKSV 367
QY 121 VHRDLAARNLVSEDLVAKVSDPGLK--FASSTLVLSKLVKWTADPAPEYFETKSV 109
DB 368 WSGVILWEVSGVGRAPYKMSLKEVSEAVEKGVKPEPDPSPGVVHIMSCWEAEPSR 427
QY 180 WSPGILLWEVSGVGRAPYKMSLKEVSEAVEKGVKPEPDPSPGVVHIMSCWEAEPSR 427
DB 428 RPPFRKIVEKLR 440
QY 240 RPSFLQIREQLEH 252

Query Match 59.6%, Score 1132, DB 1: Length 407;
Rest local similarity 57.3%; Pred No. 1,998,241;
Matches 145; Conservative 55; Mismatches 50; Indels 3; Gaps 2;

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CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC EMBL: L34542; G530158;
DB PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DB PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DB PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DB PROSITE: PS00112; SH2; 1.
DB PROSITE: PS00113; SH3; 1.
DB TRANSFERASE: TYROSINE-PROTEIN KINASE; ATP-BINDING; SH2 DOMAIN.
KW SH3 DOMAIN: PHOSPHORYLATION.
FT DOMAIN 22 69 SH3
FT DOMAIN 81 170 SH2
FT DOMAIN 194 443 SH2
FT BINDING 208 208 ATP (BY SIMILARITY).
FT BINDING 221 221 ATP (BY SIMILARITY).
FT ACT_SITE 311 311 BY SIMILARITY.
SQ SEQUENCE 467 AA. 51896 MW. 7718 P.I.

Query Match 59.6%, Score 1132, DB 1: Length 407;
Rest local similarity 57.3%; Pred No. 1,998,241;
Matches 145; Conservative 55; Mismatches 50; Indels 3; Gaps 2;

DB 190 DLGHLILGAGIGEGEFCAGVLOGEYLVQKAVYKINQNTACAFDETAFTAVKLEHNLVA 188
QY 1 NMKELKLLQIGKGEFGDVMGDPGNKVAVKCIKNDATAQAFLAASVNTQLRHSNLVQ 60
DB 250 LQGVILHH--GLYIVVHEVSKGNLVNLFRTGPAIVSTLLQALHVAEGMEVLESVK 377
QY 61 LLGVVVEEKGGIVIVTEYMAKGSIVDYLSPGSPSVLGGSCILKFSLDVCEAMVLEGNF 120
DB 308 VHRDLAARNLVSEDLVAKVSDPGLAKAEFLKGLDSSPIPVKWTAEALFNSEFSEKSV 367
QY 121 VHRDLAARNLVSEDLVAKVSDPGLK--FASSTLVLSKLVKWTADPAPEYFETKSV 109
DB 368 WSGVILWEVSGVGRAPYKMSLKEVSEAVEKGVKPEPDPSPGVVHIMSCWEAEPSR 427
QY 180 WSPGILLWEVSGVGRAPYKMSLKEVSEAVEKGVKPEPDPSPGVVHIMSCWEAEPSR 427
DB 428 RPPFRKIVEKLR 440
QY 240 RPSFLQIREQLEH 252

Query Match 59.6%, Score 1132, DB 1: Length 407;
Rest local similarity 57.3%; Pred No. 1,998,241;
Matches 145; Conservative 55; Mismatches 50; Indels 3; Gaps 2;

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174 SIKDWSFJLLWELISF3BVEYERAFILVIVUEYFVPMKZADGCTTANWVWADW 211  
DB 531 NNSPDRPFRDHFHNLENLISNSL 556  
QY 234 HLEAAMFESILOREQUELEHFKIRHL 439

RESULT 14  
ID SK22LACME STANDARD. PRT: 590 AA.  
AC P08630: P11361:  
DI 01-AUG-1988 (REL. 08, CREATED)  
DI 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)  
DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  
DE TYROSINE-PROTEIN KINASE SP029C (EC 2.7.1.112).  
GN SP029A OR SP029A OP SP02.  
US DROSOPHILA MELANOGASTER (FRUIT FLY).  
OC ECKARYOTA, METAZOA; APTRHOZOA; INSECTA; DIPTERA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 87257924.  
RA GREGORY P J, KAMMERMEYER K L, VINCENT W S, ELL WALSWORTH S G.  
KL MOL. CELL. BIOL. 7:2119-2122(1987).  
RN [2]  
RP SEQUENCE OF 356-484 FROM N.A.  
RX MEDLINE: 852115606.  
RA WALSWORTH S G, MACHAVAN K, ELLECEAU-WENIMWORTH D J.  
KL NUCLEIC ACIDS RES. 13:2153-2170(1985).  
RN [3]  
RP SIMILARITY WITH BTK SUBFAMILY.  
FA SJOHOLANDER K.  
RL UNPUBLISHED OBSERVATIONS (JUL-1997).  
CC -1- CATALYTIC ACTIVITY: ATP -> A PROTEIN TYROSINE + ADP -  
CC PROTEIN TYROSINE PHOSPHATE.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PREDOMINANTLY IN EARLY EMBRYO  
CC -1- EMBRYOGENESIS.  
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
CC DOMAIN, BELONGS TO THE BTK SUBFAMILY.  
QU EMBL: M16599; G158499; .  
DR EMBL: X02305; E1934; ALI.ERM.  
DR PIR: A27607; TVEFDS.  
DR PIR: A23051; A23051.  
DR HSSP: P06241; ISHE.  
DR FLYBASE: FBPR000302; BCK29A.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP: 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR: 1.  
DR PROSITE: PS00311; PROTEIN\_KINASE\_DOM: 1.  
DR PROSITE: PS00001; SH2: 1.  
DR PROSITE: PS00002; SH3: 1.  
DR TYROSINE-PROTEIN KINASE, PROTEIN KINASE, PHOSPHORYLATION:  
KW TRANSFERASE; ATP-BINDING, SH2 DOMAIN, SH3 DOMAIN.  
FI DOMAIN 66 92  
FI DOMAIN 145 206  
FI DOMAIN 214 307  
FI DOMAIN 330 583  
FI NP\_BIND 336 344  
FI BINDING 358 358  
FI ACT\_SITE 451 451  
FI ACT\_SITE 481 481  
FI MODRES 481 461  
FI CONFLICT 461 461  
SQ SEQUENCE 590 AA: 65887 MW: 15020625 CRC32:  
Query Match 45.68; Score 865; DB 1; Length 590  
Best Local Similarity 43.58; Pred. No. 5 90e-175;  
Matches 114; Conservative 56; Mismatches 73; Indels 0

DB 329 QLMLEELSGGFGVVRPKWNGSIDATYKMKKEGTMSDEDDLEAKVWIKL 114  
QY 4 ELKILQTIKGEGFVMDGYRGNKVAYKCKNDATAQAFLAASVWLE 114  
DB 389 YGVCTHRPILYIVIEYMKHGLNLYRKRRENTLGNMGLLEMLDGVGVWYVFRW 114

420 SOWKAEWLLNEATVNGSYFDLSONVELLEYOVNPEPPGSCPEKVKYELMPACWQW 479  
QY 234 SOWKAEWLLNEATVNGSYFDLSONVELLEYOVNPEPPGSCPEKVKYELMPACWQW 479

480 PSDRSPAEITHOAFE 494  
QY 234 PSDRSPAEITHOAFE 494

RESULT 14  
ID ABL1LACME STANDARD. PRT: 1181 AA.  
AC P03942:  
DI 01-NOV-1996 (REL. 02, CREATED)  
DI 01-NOV-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DI 01-NOV-1996 (REL. 35, LAST ANNOTATION UPDATE)  
DE TYROSINE-PROTEIN KINASE ABL1 (EC 2.7.1.112).  
GN ABL1 OR M9.  
US ABUSINUS TIGRIS (TIGER).  
OC EUMETAZOA, METAZOA; APTRHOZOA; MAMMALIA; CARNIVORA; FELIFORMIA; FELIFORMIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 8617565.  
RA GREGORY P J, KAMMERMEYER K L, VINCENT W S, ELL WALSWORTH S G.  
KL MOL. CELL. BIOL. 7:2119-2122(1987).  
RN [2]  
RP SEQUENCE OF 135-691 FROM N.A.  
RX MEDLINE: 8617565.  
RA GREGORY P J, KAMMERMEYER K L, VINCENT W S, ELL WALSWORTH S G.  
KL MOL. CELL. BIOL. 7:2119-2122(1987).  
RN [3]  
RP SIMILARITY WITH BTK SUBFAMILY.  
FA SJOHOLANDER K.  
RL UNPUBLISHED OBSERVATIONS (JUL-1997).  
CC -1- CATALYTIC ACTIVITY: ATP -> A PROTEIN TYROSINE + ADP -  
CC PROTEIN TYROSINE PHOSPHATE.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED PREDOMINANTLY IN EARLY EMBRYO  
CC -1- EMBRYOGENESIS.  
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
CC DOMAIN, BELONGS TO THE ABL SUBFAMILY.  
QU EMBL: M16599; G158499; .  
DR EMBL: X02305; E1934; ALI.ERM.  
DR PIR: A27607; TVEFDS.  
DR PIR: A23051; A23051.  
DR HSSP: P06241; ISHE.  
DR FLYBASE: FBPR000302; BCK29A.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP: 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR: 1.  
DR PROSITE: PS00311; PROTEIN\_KINASE\_DOM: 1.  
DR PROSITE: PS00001; SH2: 1.  
DR PROSITE: PS00002; SH3: 1.  
DR TYROSINE-PROTEIN KINASE, PROTEIN KINASE, PHOSPHORYLATION:  
KW TRANSFERASE; ATP-BINDING, SH2 DOMAIN, SH3 DOMAIN.  
FI DOMAIN 66 92  
FI DOMAIN 145 206  
FI DOMAIN 214 307  
FI DOMAIN 330 583  
FI NP\_BIND 336 344  
FI BINDING 358 358  
FI ACT\_SITE 451 451  
FI ACT\_SITE 481 481  
FI MODRES 481 461  
FI CONFLICT 461 461  
SQ SEQUENCE 1181 AA: 15020625 CRC32:  
Query Match 45.78; Score 868; DB 1; Length 1181  
Best Local Similarity 43.58; Pred. No. 1 80e-175;  
Matches 114; Conservative 59; Mismatches 58; Indels 0

DB 329 QLMLEELSGGFGVVRPKWNGSIDATYKMKKEGTMSDEDDLEAKVWIKL 114  
QY 4 ELKILQTIKGEGFVMDGYRGNKVAYKCKNDATAQAFLAASVWLE 114  
DB 389 YGVCTHRPILYIVIEYMKHGLNLYRKRRENTLGNMGLLEMLDGVGVWYVFRW 114



















108 163 KAWSE...KXGVSQVPRH...KXWAPGSGPFAVWMC 232  
109  
110 164 WKYDPEPTLWKLEF 503  
111  
112 165 WLLAMPSFLKGLHT 253

[illegible][illegible]

Source: Completed: Wed Jan 13 12:19:52 1999  
 File: 1001; 47 songs.